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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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The RIKEN Genome Exploration Research Group Phase II Team and the
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further details.
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                                                                                         181 gaacagcaggaccgcaatgtgcagcattaccacaagaatgagctggggtggggtgtg 240
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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602848402F1 NCI_CGAP_LU29 Mus musculus cDNA clone IMAGE:5011897 5'
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NIH-MGC http://mgc.nci.nih.gov/
NIH-MGC http://mgc.nci.nih.gov/
Ontact: Robert Strausberg, Ph.D.
Email: egapbs-femil.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
d by Life Technologies. Investigator Gilbert Smith, NIH"
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602356590F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4485071 5'
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High quality sequence stop: 632.
Location/Qualifiers
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                                                                                   1. .637
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/clone="IMAGE:5011897"
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Best Local Similarity 99.8
Matches 548; Conservative
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Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tona Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0326 row. c column: 24
High quality sequence stop: 587.
Location/Qualifiers
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/strain="FVB_N"
/db_xref="taxon:10090"
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/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH108"
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/note—"Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: 173 g 130 t
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Thssue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                            70 agtgagtggagggcctgccatccgagtgctctagccgcctggggcacccagttcgctac 129
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LLAMI1090 row: d column: 07
High quality sequence stop: 610.
Location/Qualifiers
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/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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99.8%; Pred. No. 4.2e-235;
tive 0; Mismatches 1;
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/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/note="Corgan: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI: Site_2: Sali; Cloned unidirectionally. Frimer: Oligo dr. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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602790566F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4921697 5',
BG871384
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
Plate: LLAM10840 row: d column: 18
High quality sequence stop: 585.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                 Score 475; DB 11; Length 600;
Pred. No. 4.5e-228;
0; Mismatches 1; Indels
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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602843369F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979057 5′,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/ILNL at:
http://image.lnl.gov
row: j column: 18
High quality sequence start: 3
High quality sequence stop: 634.
atgttgtttgcctgtgctcttgccttgcctcqggtctggcaacctcctgcagtttcatc
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Consortium (LLNL)
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/clone="IMAGE:4979057"
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                       /note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert 2.5 kb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCL_CGAP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
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602904343F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033867
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Pred. No. 1.5e-223;
0; Mismatches 1;
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/lab_host-"DH10B
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/db_xref="texon:10090"
/clone="IMAGE:5033867"
/clone="IMAGE:5033867"
/clone="IMAGE:5033867"
/closue_11b="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.iln.gov
Plate: LLAMI1094 row: f column: 12
High quality sequence stop: 637.
Location/Qualifiers
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Pred. No. 5.5e-214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   1. .650
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.4%;
Best Local Similarity 99.6%;
Matches 547; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgagagtga 549
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152 gcagcttctgcaacagcccggactcctgtgaacagcaggcccgcaatgtgcagcattacc 211
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Pred. No. 2.2e-198;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .842
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C2ECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5117688"
                                                                421 tgtggggtgtctcggggcttc 441
                                                                                  BI409815.1 GI:15170738
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                                                                                                                                                                                                                          mRNA sequence.
BI409815
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BI409815
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                    BE913706 1045 bp mRNA EST 29-SEP-2000 601669059F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3969014 5',
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                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Gapbs-rémail.nih.gov.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CLONE distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9146 row: e column: 15
High quality Sequence stop: 618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gibert Smith, NIH" 305 c 261 g 164 t
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                           1 (bases 1 to 1045)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 gigococgeagigagigagggcoctgccatocgagigottotagcogcotggggcacca 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcctacaacttccttattggaggacggtcatgtctatgaaggccgaggctggaacatc 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 gaacagcaggcccgcaatgtgcagcattaccacaagaatgagctgggctgggatgta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 80.3%; Score 441; DB 11; Length 1045; Best Local Similarity 100.0%; Pred. No. 6e-211; Matches 441; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3969014"
/clone=lib="NCI_CGAP_Maml"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1045
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                        BE913706.1 GI:10411594
                                                       mRNA sequence.
                                                                                                                                           Mus musculus
                                                                                                                             house mouse
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ORGANISM
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ORIGIN
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AUTHORS
TITLE
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KEYWORDS
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BE913706
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11286 row: k column: 01
High quality sequence stop: 568.
Location/Qualifiers
BI409815 842 bp mRNA EST 14-AUG-2001
602961906F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5117688 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M: Fatima Bonaldo. " 259 c 226 g 154 t 2 others
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                     1 (bases 1 to 842)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 reservisedaaccrecrecagrirearcerecececagricagregaegecerrecear
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/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
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Gaps

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3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Source irradiated bowel harvested 72 hours after irradiation (1400 Gys). Library constructed by Bob Barstead. "
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 575)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 gtgccccgcagtgagtgagggccctgccatccgagtgctctagccgcctggggcaccca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 GTGCCCCGCAGTGAGTGAGTGAGGCCCTGCCATCCGAGTGCTCTAGCCCCTGGGGCACTCCACCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                      AI507116 575 bp mRNA EST 11-MAR-1999 vj82f09.x1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:935561 3' similar to gb:X86374 M.musculus mRNA for TAG7 protein (MOUSE);, mRNA sequence.
AI507116 AI507116.1 GI:4404967
                                                                                                                                                                                                                                                                                                                                                                                                           1 atgitigititgcctgigctctccttgccctcctgggtctggcaacctcctgcagititcatc 60
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                                                                                                                                                                                                                                                                                            Length 518;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                      71.8%; Score 394; DB 10; I 100.0%; Pred. No. 2.4e-187; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 AACTICATGGACCGGGTACCCGCAAAGCGGGCCC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 aacttcatggaccgggtacccgcaaagcgggccc 394
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High quality sequence stop: 349.
Location/Qualifiers
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/dev_stage="Bowees"
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/dev_stage="Bowees"
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                                                                                                                                                                                                                                                                                                             ug52c11.yl Barstead bowel MPLRB9 Mus musculus cDNA_closs
IMAGE:1546004 5' similar to gb:X86374 M.musculus mRNA for TAG7
Protein (MOUSE);, mRNA sequence.
BE135520 GI:8598039
                                                          atgictatgaaggccgaggctggaacaicaagggigaccacacagggcccaictggaaic 331
                                                                                                                                                                                                    cctccgtgctgccctaaatcttctggaatgtggggtgtctcggggcttcctgagatcca 451
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     142 GCAGCTTCTGCAACAGCCCGGACTCCTGTGAACAGCAGGCCCGGCAATGTGCAGCATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
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High quality sequence stop: 442.
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                                                                        /note="Organ: mammary gland; Vector: pI7T3D-Pac (Pharmacia Vath a modified polylinker: Site_1: Not I; Site_2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
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601771917F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3990820 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 706).
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                1 others
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       /clone_lib="Soares_mammary_gland_NbMMG'
                                                                                                                                                                                                                                       Score 379; DB 10; I
Pred. No. 8.3e-180;
0; Mismatches 0;
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/dev_stage="4 weeks"
/lab_host="DH10B"
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'db_xref="taxon:10090"
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23 c 187 g 146 t
                                                                                                                                                                          /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3990820"
/clone=lib="NCI_CGAP_Lu29"
/fissue_Lype="spontaneous tumor, metastatic to mammary.
/lab_host="DHIOB"
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          cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LlAM3203 row: b column: 05
High quality sequence stop: 622.
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99.6%; Pred. No. 8.6e-179;
live 0; Mismatches 1;
Tissue Procurement: Gilbert Smith, Ph.D.
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4166360"
/clone="IMAGE:4166360"
/clone="IDh="NCI_CGAP_SG2"
/lab host="DH10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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NH-MGC http://mgc.nci.nih.gov/.

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://magge.llnl.gov
                BF302505 619 bp mRNA EST 21-NOV-2000 602031534F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4166360 5',
                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 2.8e-175;
0; Mismatches 1; Indels
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High quality sequence stop: 607.
Location/Qualifiers
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Matches 540; Conservative
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                                                   mRNA sequence.
BF302505
                                                                                                                         house mouse
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/db_xref="Cx7-bit/ou"
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polylinker; Site_1: Not I; Site_2: ECO RI; The
NIH_BMAP_MOB_N library is a normalized library constructed
from mouse olfactory bulbs. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dr track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
/ 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
10 q 80 t lothers
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Researchers may obtain BNAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BNAP CDNAs whose
availability will be considered under appropriate and limited
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Normalization and subtraction: two approaches to facilitate gene
488 ctctctccaggtgaccaactctatcaggtcatccaaagctgggaacactaccgaggt
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
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    .384
    /organism="Mus musculus"

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Seq primer: M13 Reverse.
Location/Qualifiers
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Fax: 301 443 9890
Email: mEST@mail.nih.gov
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Search completed: December 17, 2001, 10:01:19 Job time: 6423 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: December 17, 2001, 07:47:55; Search time 1549.8 Seconds (without alignments) Title: US-09-462-625-1 Sequence: 1 atgttgtttgcctgtgctctgggaacactaccgagagtga 549 Scoring table: IDENTITY_NC Gapext 1.0	, 537288 g chosen 300 08 45 summe	Database : EST:* 1: em_estfun:* 2: em_esthum:* 3: em_esthin:* 4: em_estpl:* 5: em_estpl:* 6: em_estpl:* 7: em_estpo:* 9: em_htc:*	estl:*est2:*btc:*btc:*bts:*gss_hun:*gss_hun:*gss_lun:*	Ouery Match Length DB ID Match Length DB ID

AA238752 my35e09.r BE199698 ug52c11.x AA238564 my35f04.r AA534993 vs17h04.r BE135520 ug52c11.y AA689693 vs03409.r AA528200 SWMECA112 AA734805 vp38b01.r AA574805 vp38b01.r AA574805 vp38b01.r AA543570 vp38b01.r AA543570 vp38b01.r AA543570 vp38b01.r AA549542 vi96d04.r BE655595 U1-M-AJ1-BG65481 602837043 BE152060 uz23h10.y AA689633 vs09908.r BE151994 uz22h10.y AA689633 vs17h10.r BF151994 uz22h10.y AA74995 vs17h10.r BF151994 uz22h10.y AA74995 vs17h10.r BF151994 uz22h10.y AA7495 vs17h10.r BF151994 uz22h10.y AA7495 vs17h10.r BF151994 uz22h10.y AA74955 vs17h10.r BF151994 uz22h10.y AA74955 vs17h10.r	117 mh22a05. 155 vo50e07. 153 ul-m-AJ1 93 vo45c05. 55 AV085455. 22 vs14g01. 04 vo45d09.
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ALIGNMENTS

AK008335 682 bp mRNA HTC 05-JUL-2001
MUS musculus adult male small intestine cDNA, RIKEN full-length
AK008335 1 G1:12842459
DS AK008335 G1:12842459
MUS musculus (strain:C57BL/6J) adult male small intestine cDNA to
cAP trapper.

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                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranaqawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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DHTGPIWNPMSIGITFWGNFWDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
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The RIKEN Genome Exploration Research Group Phase II Team and the
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
(bases 1 to 682)
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/db_xref="GI:12842460"
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BG174272 589 bp mRNA EST 06-FEB-2001
602334571F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4457680 5',
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                           121 gttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcctgt 180
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can |
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10254 row: n column: 17
                                                                                                              181 gaacagcaggcccgcaatgtgcagcattaccacaagaatgagctgggctggtgcgatgta
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Location/Qualifiers
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Query Match
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602848402F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5011897 5',
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" $174\ c\ 161\ g\ 128\ t
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                                                           ;
0
                                    Length 589;
                                               Indels
                                 Score 547.4; DB 11;
Pred. No. 1.4e-134;
0; Mismatches 1; 1
                                 99.78;
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                            Ouery Match
Best Local Similarity 99.8
Matches 548; Conservative
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DNA Sequencing by: Incyte Genomics, Inc.

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602356590F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4485071 5',
mRNA sequence.
                                                                                                                                                                                  /note="Organ: lung, Vector: pcMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"
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Plate: LLAM11062 row: c column: 02
High quality sequence stop: 632.
L. 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                           Length 637;
                                                                                                                                   /clone_lib="NCI_CGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                 1; Indels
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99.8%; Pred. No. 1.4e-134;
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LOCUS
DEFINITION
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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209 c 180 g 142 t
                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM10326 row: c column: 24
High quality sequence stop: 587.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I, Chases I to 688)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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BG244455
BG244455.1 GI:12754270
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Matches 548; Conservative
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                                                                  Mus musculus
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                VERSION
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/note="Organ: mammary; Vector: pcMv-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: 179 g 135 t
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Tennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Tennighes, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM11094 row: f column: 12

High quality sequence stop: 637.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 EST 05-JUL-2001
musculus cDNA clone IMAGE:5033867
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1 (bases 1 to 650)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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us-09-462-625-1.rst

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98.3%;
99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        BI154844 610 bp mRNA EST 05-JUL-2001
602902826F1 NIH_CGAP_MAM3 Mus musculus cDNA clone IMAGE:5032278 5'
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Itsue Procurement: Lochar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM11090 row: d column: 07
aacttcatggaccgggtacccgcaaagcgggcctccgtgctgcctaaatcttctggaa 420
                                                                                                                                                                                           490
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                                                                                                                                                                                                                tgtggggtgtctcgggggcttcctgagatccaactatgaagtcaaaggacaccgggatgtg
                                                                                                                                                                                                                                 /tissue_type="tumor, gross tissue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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Location/Qualifiers
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Mus musculus
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 600)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Heaith, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Sciurognathi; Muridae; Murinae; Mus.
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Length 610;
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DB 11;
                        Pred. No. 1.4e-132;
0; Mismatches 2;
Score 539.8;
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                                         /strain="FVB/N"
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/clone=lib="NLCGAP_SG2"
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NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                    Score 536.4; DB 11; Length 600;
Pred. No. 1.1e-131;
0; Mismatches 1; Indels 1;
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BF163190
    row: d column: 18
                                  /organism="Mus musculus"
BF163190.1 GI:11043436
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99.6%;
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    Vertebrata; Euteleostomi;
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213 c 187 g 146 t
                                                    National Institutes of Health, Mammalian Gene Collection (MGC) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caaagcactctctccaggtgaccaactctatcaggtcatccaaagctgggaacactac 540
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1
1 (bases 1 to 706)
                                                                                                                                                                                                                                                                                                                                                                                                                              //strain="czECH II (feral)"
/db_xref="taxon:10090"
/clone="INAGE:3990820"
/clone=lib="NCI_CGAP_Lu19"
/tissue_type="spontaneous tumor, metastatic feral origin."
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Pred. No. 2.2e-131;
0; Mismatches 1;
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Plate: LLAM9203 row: b column: 05
High quality sequence stop: 622.
Location/Qualifiers
1. 706
/organism-"Mus musculus"
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Matches 547; Conservative
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM11286 row: k column: 01
High quality sequence stop: 568.
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602961906F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5117688 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                     301 aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg
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602843369F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979057 5'
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NIH-MGC http://mgc.nci.nih.gov/.
541 CAAAGCACTCTCTCCAGGTGACCAACTCTATCAGGTCATCCAAAGCTGGGAACACTAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10976 row: j column: 18
                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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/clone="INAGE:4979057"
/clone=lib="NHGCAP_Mam4"
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/lab_host="DH10B"
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96.9%; Score 532.2; DB 11
Best Local Similarity 99.3%; Pred. No. 1.5e-130;
Matches 545; Conservative 0; Mismatches 3;
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Email: cgapbs-r@mail.nih.gov
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High quality sequence stop: 634.
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1. .619 /organism="Mus musculus"
             ity sequence stop: (Location/Qualifiers
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99.6%;
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Best Local Similarity 99.6
Matches 540; Conservative
             High quality
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  cccgcaatgtgcagcattaccacaagaatgagctgggctggtgcgatgtagcctacaact 250
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                  11 cctgigcictccttgccctcctgggictggcaacctcctgcagittcatcgigcccgca 70
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
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                                                                         Score 532.2; DB 11; Length 842;
Pred. No. 1.6e-130;
0; Mismatches 5; Indels 0;
                             others
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went through constructed a 259 c
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Best Local Similarity 99.1%;
Matches 534; Conservative
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/db_xref="taxon:10090"
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/lab_host="DH10B (T1 phage-resistant)"
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Not1: Site_2: Sali; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 1.5e-129;
0; Mismatches 1;
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539 accgagagtga 549
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                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

305 c 261 g 164 t
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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         1 (bases 1 to 1045)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can http://image.llnl.gov
Plate: LLAM9146 row: e column: 15
High quality sequence stop: 618.
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                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3969014"
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gb:x86374 M.musculus mRNA for TAG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3/j; double-stranded cDNA was ligated to Eco RI adaptors [GTTGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

17 c 163 g 132 t
                                                                                                                                                                        IMAGE Consortium (info@image.linl.gov) for further information.
MGI:431424
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03-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone is available royalty-free through LLNL ; contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atgttgtttgcctgtgcctccttgccctcctgggcctggcaacctcctgcagtttcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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llarity .98.7%; Pred. No. 1.9e-126;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .601
/organism="Mus musculus"
                  my35e09.rl Barstead mouse pooled clone IMAGE:697864 5' similar to
                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                           protein (MOUSE);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 499.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
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mRNA
                                                                                                AA238752.1 GI:1862775
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1 (bases 1 to 591)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.
                                                                                                                                                                                                                               92.0%;
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                                                                                                                                                             Barstead.
                                                                                                                                                                                                                                            Best Local Similarity 97.9
Matches 511; Conservative
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, F., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-NCI Mouse EST Project 1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                           ug52c11.x1 Barstead bowel MPLRB9 Mus musculus cDNA clone
IMAGE:1546004 3' similar to gb:x86374 M.musculus mRNA for TAG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
121 gitcgctacgiggigaictcacacacagccggcagcitcigcaacagcccggaciccigi
              gaacagcaggcaatgtgcagcattaccacaagaatgagctgggctggtgcatgta
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/db_xref="taxon:10090"
/clone="IMAGE:1546004"
/clone=lib="Barstead bowel MPLRB9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (MOUSE);, mRNA sequence.
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BE199698/c
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DEFINITION
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VERSION
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
Dyllinker; Site_1: ECORI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5' rand cDNA
primed with a Not I - oligo(dT) primer [5' rand cDNA
rectacharcreans considered construction and cloned and cloned and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Source irradiated bowel harvested 72 hours after
Haradiation (1400 Gys). Library constructed by Bob
Barstead. "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 2.3e-123;
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my35f04.rl Barstead mouse pooled
clone IMAGE:697855 5' similar to
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AA238564
AA238564.1 GI:1862588
            /dev_stage="8 weeks"
/lab_host="DH108"
/tissue_type="bowel"
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ë,
                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:431415
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.
Location/Qualifiers
1. 591
//crganism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                       /strain="FVB/N"
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/clone="IMAGE:697855"
/clone=lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
                                     Waterston, Wilson, Lemnou, G., Soares, B., Wilson, R. a The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marcia MyMouse EST Project WashU-HHMI Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810
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/dev_stage="7 day"
/lab_host="DH10B"
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Best Local Similarity 98.0
Matches 539; Conservative
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Sequence:

Searched:

Database

Result No.

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Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; mouse; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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AAZ19453
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    98WO-EP04287.
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23.1 1125
19.5 1110
19.3 1128
19.3 1876
14.3 1192
14.3 1192
13.8 222
12.9 521
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(without alignments)
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Duman encoding prote
Human tag7 clone c
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Bovine granulocyte
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Human full length
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ö the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, to produce and purify antibodies; to inhibit growth of mammalian tumours, prostate, colon/rectum, bladder, testis, stomach, pancaes, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo or fibro-sarcomas), melanoma or leukaemia; and as a molecular apoptosis. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; for isolating tag7 and therapeutically to inhibit or delay tumour 61 gtgcccgcagtgagtggagtgccttgccatccgagtgctctagccgcctggggcaccca 120 61 gigccccgcagigagigagggcccigccaiccgagigcictagccgcciggggcaccca 120 180 240 240 300 300 360 420 tgtggggtgtctcgggggcttcctgagatccaactatgaagtcaaaggacaccgggatgtg 480 tgtggggtgtctcgggggcttcctgagatccaactatgaagtcaaaggacaccgggatgtg 480 Gaps 9 9 1 atgitgittgcctgtgctctccttgccctcctgggtctggcaacctcctgcagtttcatc 121 gttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcctgt gaacagcaggccgcaatgtgcagcattaccacaagaatgagctgggtgcgatgta aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg aacttcatggaccgggtacccgcaaagcgggccctccgtgctgccctaaatcttctggaa ; 0 Length 549; Indels sequence encodes the murine tag7 of the invention. Sequence 549 BP; 117 A; 161 C; 151 G; 120 T; 0 other; Query Match 100.0%; Score 549; DB 20; Best Local Similarity 100.0%; Pred. No. 8.7e-156; Matches 549; Conservative 0; Mismatches 0; Claim 3; Fig 1; 138pp; English. AAT78510 standard; cDNA; cgagagtga 549 cgagagtga metastasis. This 181 301 301 361 361 421 421 481 541 541 481 AAT78510 셤 ð 8 õ 셤 à g ò g õ 셤 õ a ö 셤 g ò

Murine granulocyte peptide A precursor cDNA.

18-FEB-1998

AAT78510;

BXGXGXB

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This cDNA sequence encodes the precursor (see AAW23723) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAW23725). It was isolated from murine bone marrow cDNA using primers based on bovine BGP-A cDNA (see AAT78509). The encoded MGP-A precursor comprises signal peptide and propeptide sequences followed by 12 c-terminal amino acids corresponding to mature MGP-A. MGP-A and BGP-A (see AAW23724), exhibit activity against Gram-positive and BGP-A. (see AAW23724), exhibit activity against Gram-positive and BGP-A. (see AAW23724), exhibit activity against Gram-positive and staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxacamia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce the color of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
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                    Antimicrobial peptide; antibiotic; antibacterial; antifungal; fundicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis; endotoxaemia; mouse; ss.
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543..578
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P-PSDB; AAW23723.
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                                                                                                                                             Mus musculus
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gcctacaacttccttattggagaggacggtcatgtctatgaaggccgaggctggaacatc
                                  aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg
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99WO-US20111.
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99WO-US28634.
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29-OCT-1999;
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The present invention describes an antibody that binds to a human protein (I) selected from: PRO1361; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO1927; PRO1567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;

Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO

expression

the growth of tumors in polypeptide activity or

Claim 50; Fig 3; 226pp; English.

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anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (1) can also be detected to diagnose tumours. Agents which inhibit the activity of (1), especially the antibodies, or an antisense oligonucleotide which phybridises to genes encoding (1), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (1). AAC58019 to AAC5812 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC5812 and AAB24021 to AAB24040 represent human PRO polynucleotide and protein sequences given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                     44 cetectgeagttteategtgeecegeagtgagtggagggeeetgeeateegagtgeteta 103
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 and PR02262.
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transmembrane; secretion; immunoadhesion; pharmaceutical;
                                                                                                                                                                                                                                                                                                  Score 316.6; DB 21; Length
Pred. No. 1.1e-85;
0; Mismatches 114; Indels
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PRO4397; PRO4407; PRO1555; PRO1096; PRO2038;
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Local Similarity 77.2%;
Nes 385; Conservative
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith V,
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980S-0103314.
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980S-0103305.
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980S-0103633.
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P-PSDB; AAY99400.
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98US-0100662.
98US-0100684.
98US-0100684.
98US-0100710.
98US-0100919.
98US-0100919.
98US-0100849.
98US-0100849.
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98US-0098749
98US-0098803.
98US-0098821.
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9805-0099596.
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98US-0102484
                                             99WO-0S20111
               WO200012708-A2
  Homo sapiens.
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or

Wood WI;

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transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
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Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;

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57.7%; Score 316.6; DB 21; Length 697; llarity 77.2%; Pred. No. 1.1e-85; Conservative 0; Mismatches 114; Indels 0;
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         Best Local Similarity
Matches 385; Conserv
 Query Match
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344

gcatcaccttcatggggaacttcatggaccgggtacccgcaaagcgggccctccgtgctg

aaggacaccgggatgtgcaaagcactctctccaggtgaccaactctatcaggtcatcc

aaagctgggaacactaccg 542

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cccagggtctactggcctgcggtgtggctcaggggagccctgaggtccaactatgtgctca

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283

347 343 407 403 467 463

cetectgeagttteategtgeecegeagtgagtggagggeectgeeateegagtgeteta 103

cch 57.7%; Score 316.6; DB 22; Length 697; al Similarity 77.2%; Pred. No. 1.1e-85; 385; Conservative 0; Mismatches 114; Indels 0;

Query Match Best Local S Matches

44

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> DNA encoding protein of the invention #61 gene therapy; ВÞ DNA; 697 (first entry) 588 agaattggccacactaccg Secreted; transmembrane; AAF54356 standard; WO200078961-A1 Unidentified 02-APR-2001

18-FEB-2000; 2000WO-US04342

99US-0141037

23-JUN-1999;

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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
                                                                                                                                                                                       Fong S;
Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                  Desnoyers L, Eaton DL, Ferrara N, owski PJ, Grimaldi CJ, Gurney AL, MAA, Smith V, Stewart TA, Tumas D; PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 121; 787pp; English
                                                                                                                                                                               KP, Botstein D, Desnoy,
Goddard A, Godowski P,
Paoni NF, Roy MA, Sm
be CK, Williams PM, Wo
                                                          99WO-US28313.
99WO-US28551.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
 99US-0144758.
99US-0145698.
99WO-US20111.
                                             99US-0162506
                                                                                                                                                      (GETH ) GENENTECH INC.
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                                          29-OCT-1999;
30-NOV-1999;
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20-JUL-1999;
26-JUL-1999;
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05-JAN-2000;
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Claim 1; Figure 34; 803pp; English.
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Pred. No. 1.1e-85;
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                                                                                                                                                                melanoma; leukaemia; apoptosis inducer; human; ss.
                                                               AAX21820 standard; cDNAto mRNA; 718 BP.
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                                                                                                                                Human tag7 clone coding sequence
Query Match 57.7%;
Best Local Similarity 77.2%;
Matches 385; Conservative
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antirheumātic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AAA85576-B25593. The human secreted proteins have various activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
                                                                                                                           343
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                                 gccgaggctggaacatcaagggtgaccacacagggcccatctggaatcccatgtctattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Htag7 secreted protein gene #8.
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chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.

/*tag= a /product= PGRP-like_protein 55..117

/*tag= b 118..642 /*tag= c

sig_peptide mat_peptide WO200039327-A1

Location/Qualifiers 55..645

Homo

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dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant;
anti-inflammatory; antiarthritic; antirheumatic, dermatological;
antiproliferative; antiarteriosclerotic; anticancer; vulnerary;
cc antiviral; antibacterial; and antiquoists may be used to treat prevent cpolypetides, agonists and antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders cc e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperpoliferative disorders such as paraproteinemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and mycoarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #8 and protein sequences are represented in sequences AAR80613 and AAB25583. Sequences xx
AAA80662-A80663 represent genes related to the secreted protein gene#8.
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                                                                     cetectgcagittcatcgtgcccgcagigagtgagggccctgccaiccgagtgctcta 103
                                            9ccgaggctggaacatcaagggtgaccacacagggcccatctggaatcccatgtctattg 343
                                                                                                                                                                                                                ccctaaatcttctggaatgtggggtgtctcgggggcttcctgagatccaactatgaagtca 463
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  21; Length 726;
                   0; Mismatches 114; Indels
 Score 316.6; DB 2
Pred. No. 1.1e-85;
57.78;
77.28;
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                                                                                                                                                                                                                                                                                                                          aaagctgggaacactaccg 542
                  Matches 385; Conservative
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Query Match
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Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal

1; Fig 3; 191pp; English.

Claim

Olsen HS;

Young PE,

Rosen CA, Ruben SM, WPI; 2000-452414/39. P-PSDB; AAY96964.

(HUMA-) HUMAN GENOME SCI INC.

99WO-US30736 98US-0113809

22-DEC-1999; 23-DEC-1998;

06-JUL-2000

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               expressed by Keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 cctgctgcagccccatagtgccccggaacgagtggaaggccctggcatcagagtgcgccc 196
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                                                                                                                                                                       these profesins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TNF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human peptidoglycan recognition protein-like proteins (PGRP)
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                                                                                                                                                                                                                                                                                                                              Sequence 749 BP; 165 A; 259 C; 195 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 77.2
385; Conservative
                                                                                                                                                                                                                                                                              pulmonary fibrosis
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PGRP-C; regulator;

protein cDNA.

Chondrosarcoma peptidoglycan recognition protein-like Peptidoglycan recognition protein-like protein; PGRP;

(first entry)

31-OCT-2000

AAA51719;

BP.

AAA51719 standard; cDNA; 749

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463
                                                                                                             gcatcagcttcatgggcaactacatggatcgggtgcccacaccccaggccatccgggcag 496
                                                                                 Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA sequence encodes the precursor (see AAW23722) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated bovine granulocyte peptide A or BGP-A (see AAW33724). It was isolated from bovine borne marrow cDNA using PCR and RACE procedures. The encoded BGP-A precursor comprises a 21-amino acid signal peptide, a 156-residue propeptide and 13 C-terminal amino
                                                                    ccctaaatcttctggaatgtggggtgtctcgggggttcctgagatccaactatgaagtca
                                                                                                                                                                                                                                                                                                           Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; bovine granulocyte peptide A; BGP-A; preservative; sepsis;
                                                                                                                                                                                                                                                                                          Bowine granulocyte peptide A precursor cDNA
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29..601
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/product= BGP-A
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                                                                                                                                                                                                                            AAT78509 standard; cDNA; 688
                                                                                                                                                    524 aaagctgggaacactaccg 542
                                                                                                                                                                         agaattggccacactaccg 635
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29..91
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560..598
/*tag= c
                                                                                                                                                                                                                                                                                                                                             endotoxaemia; cattle; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-424753/39.
P-PSDB; AAW23722.
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                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
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                                                                                                                                                                                                                                                                                          Gaps
acids corresponding to mature BGP-A. BGP-A and the murine homologue, MGP-A (see AAW22725), exhibit activity against foram-logistive bacteria, fungi and viruses, specifically Staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                        gtttgcctgtgctctccttgccctcgggtct----ggcaacctcctgcagtttcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 agttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcctg
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                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                       Length 688;
                                                                                                                                                                                                                                                     Score 284.2; DB 18; Length
Pred. No. 6.4e-76;
0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 5' EST isolated from a cDNA library SEQ ID NO:308
                                                                                                                                                                                                     Sequence 688 BP; 126 A; 234 C; 201 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP,
                                                                                                                                                                                                                                                     Query Match 51.8%;
Best Local Similarity 71.6%;
Matches 389; Conservative
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AAX42265 to AAX43075 represent novel 5' expressed sequence tag (EST)
Sequences, corresponding to human secreted proteins. AAX64651 to
AAX40518 represent the EST-related proteins corresponding to AAX42265 to
AAX4052. The 5' ESTS can be used for producing secreted human gene
products. They can be used for producing secreted human gene
credions (UTRS) and upstream regulatory regions which control the
location, development stage, rate, and quantity of protein synthesis, as
well as stability of mRNA. The ESTS are also useful as probes for
chromosome mapping, and to obtain full length cDNA clones. The ESTS can
also be used in forensic procedures to identify individuals, or in
diagnostic procedures to identify individuals, or in
cause therapy protocols. The nucleic acids encoding signal peptides can be
used for directing extracellular secretion of a polypeptide or the
used for directing extracellular secretion of a polypeptide or the
into a cell. The proteins encoded by the EST sequences may be useful in
treating a variety of human conditions. Secreted proteins have
therapy proteins encoded by the EST sequences may be useful in
tho a cell. The proteins encoded by the EST sequences may be useful in
the arealing a variety of human conditions. Secreted proteins have
creating a variety of human conditions. Secreted proteins is
caniance used in the adentification of new secreted proteins is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 336; 837pp; English.
    regulation; identification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-038446/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                 Homo saptens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1998;
28-APR-1998;
                                                                                                                                                                               WO9953051-A2
                                                                                                                                                                                                                                                                                                                                                                              09-APR-1999;
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NAMES OF STREET OF STREET
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Duclert A, Giordano J;

99WO-IB00712 98US-0057719 98US-0069047 Sequence 380 BP; 67 A; 130 C; 114 G; 63 T; 6 other;

ij 44 cctcctgcagtttcatcgtgccccgcagtgagtggagggccctgccatccgagtgctcta 103 1; Score 155.6; DB 21; Length 380; Pred. No. 2.9e-37; 5; Mismatches 60; Indels 1; Query Match
28.3%;
Best Local Similarity 75.1%;
Matches 199; Conservative 5 셤

115 octgotgoagcoccatagtgoccoggaacgagtggaaggooctggcatcagagtgcgcc 174

164 acagcccggactcctgtgaacagcaggcccgcaatgtgcagcattaccacaagaatgagc 223

> g ò a ò

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283 ggccgaggctggaacatcaagggtg 307 g õ

AAD04007 standard; cDNA; 1107 RESULT 11 AAD04007

AAD04007;

(first entry) 02-JUL-2001

Human full length Zgpal cDNA #2 degenerate sequence.

Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; ADDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary, tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome 1; ss

Homo sapiens.

WO200129224-A2

26-APR-2001.

20-OCT-2000; 2000WO-US29177

20-OCT-1999; 99US-0160712. 12-JUL-2000; 2000US-0218070.

(ZYMO) ZYMOGENETICS INC.

Adler DA, Conklin DC,

WPI; 2001-290918/30

New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections

Claim 3; Page 111; 114pp; English.

GP-A) homolog, Zgpal protein. This sequence is a degenerate version of the coding region of SEQ ID NO: 7 shown in AAD4406. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for class of producing antibodies which are useful for detecting cancer. Zgpal proteins are useful for detecting cancer. Zgpal proteins are useful for detecting cancer. Zgpal carles, periodontal disease, thrush, gastrointestinal disease, uninary tract infections, respiratory infections, vaginal infections, with cystic fibrosis and prevention of infection in skin and other ceptihelial wounds. Zgpal-cytokine fusion proteins are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are useful in in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal infection and also to study epithelial call defensin induction in cell colluture. Zgpal antibodies, polynuclocides and polypeptides are useful culture. Zgpal antibodies, polynuclocides and polypeptides are useful scruture. Zgpal antibodies, polynuclocides and polypeptides are useful as diagnostics in forensis concers. Zgpal serving as markers for detecting genetic diseases or cancers. Zgpal serving and as antibodies are useful for tagging cells that express zgpal, gene zgpal gene zgpal antibodies are useful for tagging cells that express zgpal, gene zgpal general antibodies are useful for tagging cells that express zgpal, general zgpal ge expression libraries and as neutralizing antibodies or as antagonists to block zgpal activity in vitro and in vivo. Zgpal gene is also useful in This sequence is stated as encoding human truncated granulocyte peptide

Sequence 1107 BP; 186 A; 117 C; 201 G; 144 T; 459 other;

Gaps Length 1107; 9 Indels 23.1%; Score 126.8; DB 22; 38.1%; Pred. No. 2.2e-28; Live 76; Mismatches 230; , 2e-28; nes 230; Best Local Similarity 38.1 Matches 192; Conservative Query Match Best Local 3

us-09-462-625-1.rng

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Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinfilammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome 1; ss.
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                                                                                                  gcttctgcaacagcccggactcctgtgaacagcaggcccgcaatgtgcagcattaccaca 214
                                                                                                                                                    215 agaatgagctgggctggtgcgatgtagcctacaacttccttattggagaggacggtcatg 274
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12-JUL-2000; 2000US-0218070.
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This sequence is stated as encoding human truncated granulocyte peptide

(GP-A) homolog, Zgpal protein. This sequence is a degenerate version of
the coding region of SEQ ID NO: 4 shown in AADO4004. Zgpal gene is

CC located on human chromosome 1. Zgpal polypeptides are useful for
Droducing antibodies which are useful for detecting cancer. Zgpal

CC polypeptides having anti-microbial activity are useful for tracating
CC dental carries, periodontal disease, thrush, gastrointestinal disease,
CC utinary tract infections, respiratory infections, vaginal infections,
CC acquired immune deficiency syndrome (AIDS) and lung infections associated
with cystic fibrosis and prevention of infection in skin and other
CC with cystic fibrosis and prevention of infection in skin and other
CC phinelial wounds. Zgpal-cytokine fusion proteins are useful for
CC enhancing in vivo killing of target tissues (epithelial cancers, and
CC more specifically lung, ovarian and rectal cancers). Zgpal polypeptides,
CC fragments, fusion proteins or agonists are useful in in vitro studies of
CC exogenous microorganism infections such as bacterial, viral or fungal
CC infection of zgpal polypeptide, mRNA or anti-zgpal antibodies, thus
CC for detection of zgpal polypeptide, mRNA or anti-zgpal antibodies, thus
CC serving as markers for clone 5' non-coding regions of a zgpal gene. Zgpal
CC antibodies are useful for tagqing cells that express zgpal, for screening
CC antibodies are useful for tagqing cells that express zgpal, for screening
CC antibodies are useful for tagqing cells that express zgpal, for screening
CC antibodies are useful for tagqing cells that express zgpal, for screening
CC antibodies are useful for tagging cells that express zgpal, for screening
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les 230; Indels
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38.1%; Pred. No. 2.2e
ive 76; Mismatches
applications, diagnosis and treatment of gastrointestinal disease, urinary tract,
                                                                      Claim 3; Page 106-107; 114pp; English
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1094 ayathathwsnacntggccncayt 1117

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New granulocyte peptide homolog, zgpal polypeptide, for research

us-09-462-625-1.rng

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The present sequence is a cDNA encoding human full length granulocyte peptide (GP-A) homolog, Zgpal protein. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries.

The periodontal disease, thrush, gastrointestinal disease, urinary tract infections, respiratory infections, raginal infections, acquired immune deficiency syndrome (AIDS) and lung infections associated with cystic Zgpal-cytokine fusion proteins are useful for enhancing in vioc killing of target tissues (epithelial cancers, and more specifically lung, covarian and rectal cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are useful in in vitro studies of exogenous control of the proteins or agonists are useful in in vitro studies of exogenous control of proteins with a sacterial, viral or fungal infection and also to study epithelial cell defensin induction in cell culture. Zgpal antibodies, polymocleotides and polypeptides are useful for detection of zgpal polypeptide, mRNA or anti-zgpal antibodies, thus serving as markers for detecting genetic diseases or cancers. Zgpal sequences are useful as a diagnostics in forensic DNA profiling and as probes or primers to clone
                                                                                                                                                   Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product "Mature human full length zgpal protein #2"
                                                                                                                                                                                                                                                                                                                                                                                      full length zgpal protein #2 with
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                                                                                                           Human full length granulocyte peptide homolog Zgpal cDNA #2.
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AAD04006 standard; cDNA; 1110
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52..1107
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5' non-coding regions of a zgpal gene. Zgpal antibodies are useful for tagging cells that express zgpal, for screening expression libraries and as neutralizing antibodies or as antagonists to block zgpal activity in vitro and in vivo. Zgpal gene is also useful in gene therapy.
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/product= "Human full length zgpal protein #1 with
linker sequence"
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                                                                                                                                                                                                                                                                  Length 1110;
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                                                                                                                                                                  Sequence 1110 BP; 249 A; 319 C; 295 G; 247 T; 0 other,
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c peptide (GP-A) homolog, gapal protein. Zapal gene is located on human chromosome 1. Zapal protein. Zapal gene is located on human chromosome 1. Zapal polypeptides are useful for producing antibodies chromosome 1. Zapal polypeptides having chromosome 1. Zapal polypeptides having chromosome 1. Zapal polypeptides having anti-microbial activity are useful for treating dental carries.

Competions, respiratory infections, vaginal infections, acquired immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infection in skin and other epithelial wounds. Competitions are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zapal polypeptides, fragments, fusion proteins are useful in in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal infection and also to study epithelial cell defensin induction in cell culture. Zapal antibodies, polymelectides and polypeptides are useful for detection of antibodies, polymelectides and polypeptides are useful for detection of cappal polypeptide, mRNA or anti-zapal antibodies, thus serving as markers for detecting genetic diseases or cancers. Zapal sequences are useful for cappal appropriates are useful for cappal antibodies are useful for cappal, for screening expression libraries and as neutralizing antibodies or as antagonists to block zapal activity in vitro and in vivo. Zapal gene is also useful in gene therapy.
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/product= "Mature human full length zgpal protein #1"
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2000US-0218070
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Matches 243; Conservative
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P-PSDB; AAE00692.
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12-JUL-2000;
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Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-W) are discused. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in ammmal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antegonists directed against these proteins may be useful in reducing or eliminating disorders such as sendotoxic shock and autoimnume disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                     Wound healing tissue peptidoglycan recognition protein-like protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidoglycan recognition protein-like protein; PGRP; PGRP-W; regulator; wound healing tissue; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
                                                                 978 ggcagcccaagacctgatccagtgtgccatggtcaaagggtacctgactcccaactacct 1037
                                                                                                                                     1038 gctggtgggccacagtgatgtggcccgaaccttgtctcctgggcaggctttgtacaacat 1097
                                399 tgotgocotaaatottotggaatgtggggtgtotogggggottootgagatocaactatga 458
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918 cctgggcattaccttcatgggcaccttcacaggtataccacccaatgctgcagcactaga 977
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107..1213
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158..1210
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P-PSDB; AAY96963.
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CC pulmonary fibrosis.

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SQ Sequence 1876 BP; 422 A; 545 C; 439 G; 470 T; 0 other;

Query Match

Query Match

Bost Local Similarity 53.9%; Pred. No. 5.8e-22;

Matches 240; Conservative 0; Mismatches 202; Indels 3; Gaps 1;
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465 aggacaccgggatgtgcaaagcactctctccaggtgaccaactctatcaggtcatcca 524

Search completed: December 17, 2001, 09:35:26 Job time: 6376 sec

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.5 ompugen Ltd. Search time 22.96 Seconds (without alignments)	6 Million cell updates/sec		473505				yy chance to have a we result being printed, distribution.	Description	088593 mus musculu 075594 homo sapien Q951n4 rattus norv Q99kl2 camelus dro 076537 trichoplusi Q99ks camelus dro 076537 trichoplusi Q99kx7 drosophila Q9vx7 drosophila Q9v4q4 drosophila Q17188 bombyx mori Q9v4q4 drosophila Q9v4q4 drosophila Q9vqq drosophila Q9vqq drosophila Q9vqq drosophila Q9vqq drosophila Q9vqqq drosophila Q9vqq drosophila Q9vqqq drosophila Q9vqqq drosophila Q9vqqq drosophila Q9vqq drosophila Q
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09584 bombyx mori
09577 saccharomyc
09577 saccharomyc
07281 arabidopsis
07281 chimpanzee
07369 abcillus ha
02201 chimpanzee
07369 sachpodes et
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09907 arabidopsis
09141 oryctolagus
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09917 xylelma fas
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0914m8 pseudomonas
0904k7 mus musculu
P95734 staphylococ
09cwv5 mus musculu
0917f4 drosophila
          Q9etp3 corynebacte
Qaw73 quillardia
P78720 orpinomyces
Qawr2 oryza sativ
Q48591 arabidopsis
O47143 calluna vul
O47146 erica austr
O47122 lyonia oval
Q47122 lyonia oval
Q95900 xenopus lae
Q95917 arabidopsis
Q9117 arabidopsis
Q91899 schizosacch
Q4850 arabidopsis
Q9682 arabidopsis
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0995c5 pirital vir
09ku64 vibrio chol
014000 schizosacch
09n3e8 caenorhabdi
093990 candida alb
075178 homo sapien
09fi80 arabidopsis
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O95064 homo sapien
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ALIGNMENTS

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RESULT 1
088593
ID 088593 PRELIMINARY; PRT; 182 AA.
AC 088593; Q62185;
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DF PEPTIDOGLYCAN RECGGNITION PROTEIN PRECURSOR.
GN PGLYRP OR PGRP OR TAG7.
OS Mus musculus (Mouse).
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A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K.; Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Radota K., Matsuda H.S., Nikaido I., Rochiwa H.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Whyshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
A Whyshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
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-1 TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SPLEEN AND LUNG. ALSO DETECTED IN BRAIN AND THYMUS. IN THE LUNG, EXPRESSED IN THE PORKINJE CELLS INTRAALVEOLAR SPACE, IN THE BRAIN, EXPRESSED IN THE PORKINJE CELLS OF THE CEREBELLUM AND IN CERTAIN LAYERS OF NEURONS IN THE HIPPEOCAMPUS. ALSO DETECTED IN CELLS FILLING THE SPACE WITHIN THE INTESTINAL VILLUS.

-1 SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                               Kang D., Liu G., Lundstroem A., Gelius E., Steiner H.;
"A peptidoglycan recognition protein in innate immunity conserved from insects to humans.";
Proc. Natl. Acad. Sci. U.S.A. 95:10078-10082(1998).
                                                                                                                                                                                                                                                      EGUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.

KISELINE—99325081; PubMed—9660837;

KISELION S. K. Kustikova O.S., Georgiev G.P.;

Kabishev A.A., Lukandian E.M., Georgiev G.P.;

Molecular cloning and characterization of the mouse tag7 gene codding a novel cytokine.";

T. Biol. Chem. 273:18633-18639(1998).

S. Balot. Chem. 273:18633-18639(1998).

S. Sauguence FROM N.A.

Slayton W.B., Rigaa A., Hancock J.D., Zaugg J.K., Le T.V.,

Trautman M.S., Spangrude G.J., Carroll W.L., Schibler K.R.;

T. "Granulocyte-colony stimulating factor up-regulates expression of murine tag7 during myeloid differentiation.";

Submitted (OCT-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
MEDLINE-2108566.
ABDLINE-2108566.
Shibata K., Yosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF076482; AAC31821.1; -.
EMBL; AF193843; AAF06335.1; -.
EMBL; AK008335; BAB25611.1; -.
EMBL; BC005582; AAH05582.1; -.
EMBL; X86374; CAA60133.1; ALT_SEQ.
EMBL; Y12088; CAA72803.1; -.
                                                                                                                 TISSUE-SPLEEN; ... MEDLINE-98374308; PubMed-9707603;
    Chordata;
Rodentia;
    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Query Match
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09JLN4;
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09GK12
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                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wan T., Zhang W., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN AND IS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                         100.0%; Score 118; DB 11; Length 182; 100.0%; Pred. No. 2e-11; Live 0; Mismatches 0; Indels 0
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PEPTIDOGLYCAN RECOGNITION PROTEIN.
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D954C51440DC27DC CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 95:10078-10082(1998)
         . Pglyrp. Cytokine; Apoptosis; Signal.
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                                                                                                                                  POTENTIAL
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20489 MW;
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Best Local Similarity 100.0
Matches 21; Conservative
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182 AA;
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MGD; MGI:1345092;
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196 AA;
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                                 Immune response;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
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TISSUB-LACTATING MAMMARY GLAND;
Kappelar S.R., Farah Z., Puhan Z.;
Wallk as a Source of Camel (Camel Granelus Peptidoglycan Recognition Protein.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131676; CAC19553.1;
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PEPTIDOGLYCAN RECOGNITION PROTEIN.
B6A1BD818030A7CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rehman A., Teodecki E.E., Krueger J.M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154114; AAF73252.1;
SEQUENCE 183 AA; 20590 MW; 5B9C1B7AA8A2EC21 CRC64;
                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PEPTIDOGLYCAN RECOGNITION PROTEIN PGRP.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.
      DB 4; I
3.1e-06;
                                                                                                                                                                                                                          183 AA.
  Score 86; DB Pred. No. 3.1e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                 21
                                                                                                  68 NTPASCQQQARNVQHYHMKTL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 21 PC
22 193 PI
193 AA; 21377 MW;
72.98;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 SSPDSCEQQARNVQLYQMKQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NSPDSCEQQARNVQHYHKNEL 21
                                                                           1 NSPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSPDSCEQQARNVQHYHKNEL
              Local Similarity 71.4 tes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4
Matches 15, Conservative
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Loca 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9838;
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Interpro; IPR002405; Inhibin_alpha.
Interpro; IPR001839; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                   4 DSCEQQARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C33D9.5 PROTEIN.
C33D9.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VXX7
Q9VXX7;
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q18378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q9VXX7
ID Q9
AC Q9
DT 01
         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LARVA;
MEDLINE-98374308; PubMed-9707603;
Kang D., Liu G., Lundstroem A., Gelius E., Steiner H.;
"A peptidoglycan recognition protein in innate immunity conserved from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insects to humans.";
Proc. Natl. Acad. Sci. U.S.A. 95:10078-10082(1998).
-!- FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN AND TRIGGERS THE PROPENOLOXIDASE CASCADE WHICH IS AN IMPORTANT INSECT INNATE IMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                            Trichoplusia ni (Cabbage looper).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Noctuoidea, Noctuidae, Plusiinae, Trichoplusia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN FAT BODY WITH WEAK EXPRESSION DESERVED IN HEMOCYTE. NO EXPRESSION DETECTED IN GUT.
-1- INDUCTION: BY BACTERIAL CHALLENGE.
-1- SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kapanen A.I., Ryhanen J., Birr E., Vaananen H.K., Tuukkanen J.K.; "Decalcified reindeer antler matrix as bone inducing agent."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO THE TGF-BETA FAMILY.
EMBL; AF300813; AAG22543.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDOGLYCAN RECOGNITION PROTEIN. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 17-21, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.1%; Score 52; DB 5; Length 182; ilarity 42.9%; Pred. No. 0.86; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
56631E762AE34794 CRC64;
                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) BONE MORPHOGENETIC PROTEIN 3B (FRAGMENT).
                                                                                                                             182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 AA.
                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Odocoileinae; Rangifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF076481; AAC31820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20572 MW;
DIPASCAQQAQNVQSYHVRNL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NSPDSCEQQARNVQHYHKNEL 21
                                                                                                                                                                   (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rangifer tarandus tarandus.
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immune response; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCBI_TaxID-86329;
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7111;
                                                                                                                                                                   01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cervidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSCICE;
                                                                                                                        076537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGNAL
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                  99
                                                                               RESULT
076537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Laister L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 523;
                                                                                                                                                                                                                                                                        Length 440;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lloyd C.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                          PRINTS; PR00669; INHIBINA.
Prodom; PD000357; TGF-beta; 1.
SMART; SM0204; TGF1: 1.
PROSITE; PS00250; TGF_BETA; 1.
Glycoprotein. 1 1 1 1 1 SEQUENCE 440 AA; 48669 MW; 97E96AFCBA23F99A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
EMBL; Z68159; CAA92288.1; -.
SEQUENCE 523 AA; 61174 MW; 6CBEDECE717B8873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 41.1%; Score 48.5; DB Best Local Similarity 32.1%; Pred. No. 8.5; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                      Score 50; DB 6
Pred. No. 4.1;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Created)
05, Last sequ
13, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PDSCEQQARNVQHY------HKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                      42.4%;
ilarity 50.0%;
Conservative
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 269 DERPEHAPHAQHYHKHEL 286
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Last sequence update) Last annotation update)

Created) PRT;

696 AA.

PRELIMINARY;

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R. SELDENCE FROM N.A.

R. STRAIN-BERKELES;

R. MEDLINE-2-1095006; pubmed-10731132;

R. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

R. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

R. Adams M.D., Celniker S.E., Holt R.A., Fashburner M.; Henderson S.N.,

R. Gerge R.A., Lewis S.E., Richards S., Ashburner M.; Henderson S.N.,

R. Sutton G.G., Worthman J.R., Yandell M.D., Zhang O., Chen L.X.,

R. Barlon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

R. Barlon R.Y., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Ballew R.M., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Ballew R.M., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Ballew R.W., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Ballew R.W., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Ballew R.W., Basu A., Baxendale J., Bayraktarolon C.R., Miklos G.L.G.,

R. Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahako S.,

R. Borkova D., Botchan M.R., Buuller H., Cadieu E., Center A., Chandra I.,

R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

R. Dodson K., Goor F., Garrell J.H., Gu Z., Gunn P., Harris M.,

R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hourk J.,

R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

R. Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibeyam C.,

R. Harris N.L., Harvey D., Heiman T.J., Well M.-H., Ibeyam C.,

R. Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibeyam C.,

R. Harris N.L., Marvey D., Heiman T.J., Well M.-H., Ibeyam C.,

R. Janko P., Lel J., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

R. Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,

R. Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,

R. Spier E., Spradling A.C., Standers R., Weller E., Spradling A.C., Standers R., Weller B., Walliams S.M.,
                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                               ...war-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 0315702 PROTEIN.
                                                                                                            09V7M0;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro
                                                                                     0977M0
                                            RESULT
                                                                   09V7M0
                                                                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richerlas S., Asbuurnen W., Henderson S.N.,
RA Button G.W., Worturn J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Bager R.G., Helt G., Walson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Prannkoch C., Baldwin D.,
RA Ballew R.M. Basu A., Baxendalle J., Bayraktaroon C.R., Miklos G.L.G.,
RA Ballew R.W., Basu A., Baren B.P., Bhandari D., Bolshakov S.,
RA Borkvar D., Botchan M.R., Bouck J., Barokstein P., Beroktier P.,
RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davise P.M.,
RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davise P.M.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Pletz S.M.,
RA Dodson K., Cong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.L.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Harris M.L.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Mutphy B., Murphy L., Mazny D.M., Nelson D.L.
RA Merkulov G., Milshina N.V., Nubbarry C., Morris J., Moshrefi A.,
RA Holson D.R., Nelson K.A., Li J.J., Li Z., Liang Y., Lin X.,
RA Holson D.R., Nelson K.A., Mixon K., Wolsker D.M., Nelson D.L.,
RA Relnert K., Remington K., Saudhers R., Sun E.,
Ra Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Shue B.C., Sident-Kiamos I., Simpson M., Strong R., Sun E.,
RA Harsa R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Wellsenbelder F., Shan R.,
Ra Hellams R. B., Wolder Y., Sun E.,
Ra Harsa R., Tector C., Turner R., Venter E., Wang S., Lao Q., Zhao Q., Zh
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CG11709 PROTEIN (PEPTIDOGLYCAN-RECOGNITION PROTEIN-SA).
PGRP-SA OR CG11709.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephygroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-DP CL CN BW;
MEDLINE-20538582; PubMed-11106397;
Werner T., Liu G., Kang D., Ekengren S., Steiner H., Hultmark D.;
"A family of peptidoglycan recognition proteins in the fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AA; 22260 MW; D200A6EA79C66731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.";
Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000).
EMBL; AE003486; AAF48056.1; -.
                                                                                                                                                                                                                         STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF207541; AAG23735.1; -. AF207540; AAG23734.1; -.
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                           NCBI_TaxID=7227;
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                                                                                    Length 696
                                                                                                               Indels
                                        696 AA; 79759 MW; 7BC2620B01FAE816 CRC64;
                                                                                39.8%; Score 47; DB 5; 40.0%; Pred. No. 19;
                                                                                                               Mismatches
                         FBgn0034101; CG15702.
Science 287:2185-2195(2000).
                                                                                                                                        21
                                                                                                                                                               61 TPDQVELQVLGLRHYYSKEL 80
                                                                                                                                     2 SPDSCEQQARNVQHYHKNEL
                                                                             Query Match
Best Local Similarity 40.0
Matches 8; Conservative
              EMBL; AE003807;
                              FlyBase;
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RESULT Q17188

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Gaps

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40.7%; Score 48; DB 5; Length 203; 50.0%; Pred. No. 4.2; Live 4; Mismatches 4; Indels

Conservative

Query Match Best Local Similarity Matches 8; Conservat

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39.0%;
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Best Local Similarity 41.8.
To Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HCT9
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Q9HCT9
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09VDQ.
09VDQ.
09VDQ.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG4413 PROTEIN.
CG4413 Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Prerygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., George R.A., Lewis S.E., Fichards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Beason K.Y., Benos P.V., Barendale J., Bayaktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
           017188;
01-NOV-1996 (TERMELrel. 01, Created)
01-NOV-1996 (TERMELrel. 01, Last sequence update)
01-JUN-2001 (TERMELrel. 17, Last annotation update)
ANTENDAPEDIA HOMOLOGUE PROTEIN.
BOMDAX MOLI (SILK moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
NCBI_TAXID-7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-KINSHU X SHOWA; TISSUE-MIDDLE SILK GLAND;
Magata T., Kohji U., Chi-chung H., Xin X., Fukuta M., Suzuki Y.;
"Segmental identification and silk gland expression of the Bombyx
Antennapedia homologue gene.";
Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.0%; Score 46; DB 5; Length 259; 50.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEDBOX_1; 1.
PROSITE; PS50071; HOMEDBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 259 AA; 29916 MW; C3EAE005C370F310 CRC64;
  259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D16684; BAA04087.1;
HSSP; P02833; 1HOM.
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Best Local Similarity 50.0
Matches 7; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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09VDQ4
SWERN DRANGE CONTRACTOR OF THE PROPERTY OF THE
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RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.W.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.W., Glasser K.,

RA Harris N.L., Harvey D., Heinan T.J., Harris M.,

RA Harris N.L., Harvey D., Heinan T.J., Wennison J.A., Ketchum K.A.,

Balali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Malush R., Morbay D., Murphy D., Lai Z.,

Liu X., Mattel B. L., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B. M., Murphy B., Murphy D.M., Nelson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Porleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Sylfskas R., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Jeney X.H., Zhong F.N., Zhong W., Zhon G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao K.A., Myers E.W., Rubin G. M., Venter E., Wang S., Yao Q., Zheng T., The genome sequence of Drosophila melanogaster.",

RA Zheng X.H., Myers E.W., Rubin G. M., Venter J.C.;

RHENE, REME, REME, REMES, ARFS5756:1;

RHENE, REME, REMES, RAFS5756:1;

RHENE, REME, REMES, REME
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Usukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-20407466; PubMed-10947988;
St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
Kinzler K.W.;
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W; 6BlDlD6AA353830A CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TUMOR ENDOTHELIAL MARKER 7 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
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InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMARY; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DNA-DIAGING; Metal-binding; Zinc_finger
SEQUENCE 402 AA; 45857 MW; 6B1D1D6AA3
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Pred. No.
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EMBL, AF279144; AAG00869.1; -.
InterPro; IPR003886; Nidogen_ext.
InterPro; IPR002165; Plexin_repeat.
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RESULT Q39795

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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.
RA Broilser L., Brans A., Bran M., Brignell S.C., Bron S.,
Broulllet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broulllet S., Errington J., Fabret C., Ferrari E., Poulger D.,
Entian K.D., Errington J., Fabret C., Ferrari E., Poulger D.,
RA Glins S.Y. Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,
RA Kuita K., Eaplaus A., Eardinois S., Kuan M., Jones L.,
RA Kuita K., Lapidus A., Lardinois S., Lauber J., Lazaretc V.
RA Kuita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Kuita K., Lapidus A., Lardinois S., Rauber J., Lazaretc V.,
RA Ruita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S. H.,
RA Presecan E., Pujic P., Purnelle B., Ropport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Rapport G., Rey M., Reynolds S.,
RA Schjuchi J., Sekowska A., Seros S.J., Senror P., Soin B.,
RA Schotti J., Scholetch S., Schroeter R., Scoffone F.,
RA Schotti A., Tanakoshi A., Tanaka T., Tarahashi H., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Tosato P., Wolher E., Wedler E., Wedler H., Weitzenegger T.,
RA Tosato P., Wolhikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
RA Toshilake Genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.1%; Score 45; DB 2; Length 143; 40.0%; Pred. No. 9.2; tive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 299112; CAB13575.1; ...
Complete proteome.
SEQUENCE 143 AA; 16166 MW; 750A24D99B463C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, C3
01-MAY-2000 (TrEMBLrel. 13, L6
01-MAY-2001 (TrEMBLrel. 17, L6
CG10148 PROTEIN.
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Best Local Similarity 40.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
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Q9VFY8
                             ογ
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                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
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                                                                                                                                                                        39.0%; Score 46; DB 4; Length 502; 45.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 38.1%; Score 45; DB 10; Length 139; Best Local Similarity 45.8%; Pred. No. 9; Matches 11; Conservative 1; Mismatches 6; Indels
                                                                                                    TUMOR ENDOTHELIAL MARKER 7.
94E0AE815B296144 CRC64;
                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
2S ALBUMIN STORAGE PROTEIN.
2S ALBUMIN STORAGE PROTEIN.
02ACE24FFEC9EF90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galau G.A., Wang H.Y.C., Hughes D.W.;
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M86213; AAA33066.1;
Mendel; 8406; Goshi; 2374; 8406.
                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2S ALBUMIN STORAGE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                  139 AA
                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001768; Cereal_tryp_amyl_inh.
InterPro; IPR003612; AAI.
                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
Pfam; PF01437; Plexin_repeat; 1.
                                                                               18 PO
502 TU
55647 MW;
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59 2S
139 2S
15700 MW;
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                     SMART; SM00539; NIDO; 1
SMART; SM00423; PSI; 1.
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                                                                                                              502 AA;
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Best Local Similarity
Matches 9; Conserv
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SIGNAL
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Gaps

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RESULT 14

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RA SULTON G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Ra Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Bridon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Abril J.F., Adpayani A., An Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Borkova D., Botcham M.R., Bouck J., Barokstein P., Bottlier B.M.
Borkova D., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtls K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plankov B.C., Dunn P.,
RA Double M. Davies M. S., Garg N.S., Galbart W.M., Glasser K.,
RA Dodson K., Doup L.E., Downes M., S., Galbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Jalail M., Kalush F., Karpen G.Y., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., Molntosh T.C., McLeod M.P., Mobsheefi R.,
RA Lasko P., Leil Y., Leitjisky A.B., Li J., Li Z., Liang Y., Lin X.,
Muttei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Luu X., Mattei B., Molntosh T.C., Molskern D.R., Pacleb J.M.,
Ralazolo M., Pittman G.S., Pan S., Pollard J., Moshrefi R.,
Reinert K., Remington K.A., Musphy B., Murphy L., Weissenbach J.,
Rales B.C., Siden Kalmos I., Simpson M., Stupski M.P., Smith T.,
Spier E., Sprading A.C., Stapleton M., Stupski M.P., Smith T.,
Rabeng X.H., Zhong F., Weinstook G. M., Weissenbach J.,
Rabeng X.H., Zhong W., Ruinstock G. M., Weissenbach J.,
The genome sequence of Drosophila melanogaster.", Sidu X., Smith H.D.,
Resell. Agon 3608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 5; Length 329;
Pred. No. 20;
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SMART; SM00369; LRR_TYP; 1.
200 Aa; 37165 MW; C4106348E5C334DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE003699, AAF54907.17.
FLYBASE, FB970038120, CG10148.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
InterPro; IPR003593; LRR_typ.
Pfam.; PF00560; LRR; 4.
PRINTS; PR005019; LEURICHRPT.
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Best Local Similarity 47.68
Matches 10; Conservative
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38.1%; Score 45; DB 2; Length 604; 50.0%; Pred. No. 36; 1; Mismatches 7; Indels

Best Local Similarity 50.0 Matches 8; Conservative

Query Match

484 PDVCAQGTRGVTHRHE 499

PRELIMINARY;

Q9Y3R1; Q9Y3R1 RESULT 17

09¥3R1

3 PDSCEQQARNVQHYHK 18

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; MAO1. Microbiol. 21:77-96(1996). EMBL; AL109962; CAB53151.1; ...

11 protein. 604 AA; 68234 MW; 94450B691F008FD3 CRC64;

Hypothetical

SEQUENCE

Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

STRAIN=A3(2); MEDLINE=97000351; PubMed=8843436;

FROM N.A.

SEQUENCE

STRAIN-A3(2); Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases

SEQUENCE FROM N.A.

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BUCCI (C., Chiariello M., Lattero D., Maiorano M., Bruni C.B.;
Bucci (C., Chiariello M., Lattero D., Maiorano M., Bruni C.B.;
"Interaction cloning and characterization of the cDNA encoding the human prenylated rab acceptor (PRA1).";
Biochem. Biophys. Res. Commun. 258:657-662(1999).
                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 4; Length 185;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                         185 AA; 20706 MW; ACSFD5B9CB6C23E4 CRC64;
                                            Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA
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                  01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequ 01-NOV-1999 (TrEMBLrel. 12. Tast and
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                                          01-NOV-1999 (TrEMBLrel. 12, Last s
01-NOV-1999 (TrEMBLrel. 12, Last a
PRENYLATED RAB ACCEPTOR 1 (PRA1).
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Best Local Similarity 36.8%;
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Q9UI14;
01-MAY-2000 (TEMBLEE], 13,
01-MAY-2000 (TEMBLEE], 13,
01-MAY-2000 (TEMBLEE], 13,
                                                                                                                                                                                                                                                                                                                                                                                                                     1 NSPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                         59 NLGELCQRLVRNVEYYQSN 77
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                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q9UI14
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Matches
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Gaps

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Indels

10;

Mismatches

ð 셤 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.

Streptomyces coelicolor.

RESULT 16
09RIY1
AC 09RIY1;
DT 01-MAYDT 01-WAYDT 01-WAYDE HYPOTHE
GN SCJI.33
GN SCJI.33
GN ACLEDIO
OC ACLIDO
OX NCBL TR
RN [1]
RR SEQUENC
RA SEQUENC
RA SEGOEN
RA SEGOEN
RA SEGOEN

SEQUENCE FROM N.A. STRAIN-A3(2); Seeger K.J., Harris D.;

NCBI_TaxID-1902;

01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 68.2 KDA PROTEIN.

604 AA.

PRT;

PRELIMINARY;

Q9RIY1;

Q9RIY1

us-09-462-625-2_copy_55_75.rspt

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Ouery Match
Best Local Similarity
Matches 7; Conserv
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Q40513
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                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                               Jin W., Huang C., W., T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y., Han Z., Wang Y., Chen Z., Fu G., Anovel gene expressed in human hypothalamus."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL. AF112202; AAF17190.1; SEQUENCE 185 AA; 20648 MW; A85BD5BDCF6C23E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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"Specific interaction of Dexras with prenylated rab acceptor 1
                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 185;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 11; Length 185;
Pred. No. 17;
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J. Blol. Chem. 272:0-0(1997).
EMBL; AF025506; AABB1721.1;
SEQUENCE 185 AA: 20643 MW; DA6341AE66F5C2F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TEMBLrel. 05, Last annotation update)
PRENYLATED RAB ACCEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PRENYLATED RAB ACCEPTOR 1 (2310040106RIK PROTEIN).
RABACI OR PRAI OR PRA OR 2310040106RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 AA
                                                                                                                                                                                                                                                                                                            5; Mismatches
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Best Local Similarity 36.8%;
Matches 7; Conservative
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Best Local Similarity 36.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
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                                                               TISSUE-HYPOTHALAMUS;
                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
    NCBI_TaxID-9606;
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035394
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

STRAIN-CS7BL/6J; TISSUE-TONGUE, AND SWALL INTESTINE;

X MEDLINE-21085660; Pubmed-11217851;

XA ALZAWA T., BATA A., FURUNISHI Y., YOSHINO M., Itoh M., Ishii Y.,

RA ALZAWA K., IZAWA M., NISHI K., KIYOSAWA H., KAGCHI J., FURUGA S.,

RA SAITO T., OKAZAKI Y., GOJODOTI T., BONO H., KASKWAWA T., SAITO R.,

RA FISCHMANN W., GASTERIANG T., GISSI C., KING B., KOCHIWA H.,

RA SCHIMI L.M., STAUDI F., SUZUKI R., TOMITA M., WAGNET T., WASKI K., OKIGO T., FULUD M., AONO H., BADAGATELLI R., BATSH G.,

RA SCHIMI L.M., STAUDI F., SUZUKI R., TOMITA M., GAIDOLIGI M.,

RA SCHIMI L.M., SAUDI F., SUZUKI R., TOMITA M., GAIDOLIGI M.,

RA BLOWNSTEAN M.J., Bult C., FletCher C., Fulita M., GAIDOLIG M.,

RA LYONS P., MATCHIONI L., MASHIMA J., MAZZATELLI J., MOMDAGETS P.,

RA SCHOR P., RING B., KINGWALD M., ROCATIGNE T., SASAMONOON N.,

RA SSSAKI H., SATO K., SCHOGNDACH C., SEYA T., SINDATA Y., STONOH K.-F.,

RA SUZUKI H., TOYO-OKA K., WANG K.H., Weitz C., Whittaker C., Wilming L.,

RA HAVSAHYZAKI Y., TOYO-OKA K., WANG K., RASEGWAN T., KAWAJI H., KOHTSUKI S.,
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WA MEDLINE-97048712; PubMed-8893543;
A Davies, Di Rosa, Eneva T., Saedler, Sommer;
A Davies, Di Rosa, Eneva T., Saedler, Sommer;
T. "Alteration of tobacco floral organ identity by expression of combinations of Antirrhaum MADS-box genes.";
T. Tombinations of Antirrhaum MADS-box genes.";
T. SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
T. SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
TRANSFAC; T03109;
TRANSFAC; T03109;
TRANSFAC; T03109;
THEAPTO; IPR002487; K-box.
THEFPTO; IPR002100; MADS-box.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional annotation of a full-length mouse cDNA collection.";
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"Mouse prenylated Rab acceptor (mPRA).";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20619 MW; 86C82C0502B5CB5B CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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MGD; MGI:1914946; 2310040106Rik
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EMBL; AF252856; AAF68476.1;
EMBL; AK009726; BAB26465.1;
EMBL; AK00859; BAB25744.1;
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RX PEDCENCER FROM N.A.

RA Adams M.D.C. Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D.C. Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,

Ananatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

Anders M.D.C. Leavis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gorger R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffer B.D.,

And R.H., Agbayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Besson R.Y., Beans P.W., Berman B.P., Bhandari D., Bolshakov S.,

Burkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,

Burkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Bastlets P.M.,

Burkova D., Botchan M.R., Bouck J., Brokstein P., Barotkier D.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Center A., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plukovo B.C., Dunn P.,

Burbin K.J. Evapelista C.C., Ferraz C., Ferriers S., Plakschman W.,

RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

A Glodek A., Gong F. Gorrell J.H., Gu Z., Glann P., Harris M.L., Harvey D., Heilman T.J., Hernandez J.R., Houck J.,

A Jalali M., Kalush F., Kalven G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lux Matteil B.L. McIntosh T.C., McLeod M.P., McPherson D.,

Mult S.M. Woyn W. Wurphy B., Murphy L., Murzny D.M., Nelson D.L.,

Raber D., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Alux Matteil B., McIntosh T.C., McLeod M.P., Perly W., Resen M.C.,

Raber D., Lei Y., Mayers B.M., Wursny D.M., Nelson D.L.,

Raber D., Spradling A.C., Stapleton M., Strong R., Sun B.,

Syliekas R., Massarman D.A., Weilspon W., Stupski M., Wang S., Yun S.,

Raber D., Zhong Y., Lankow W., Wang S., Pan W., Wang S., Yao, O. W.,

Syliekas R., Lakon W., Wang S., Pan S., Pollard J., Putl, Wang S., Yao, O. W.,

Syliekas R., Lakon W., Wang S., Mun Wang S., Yao, W.,

Raben S., Wang S., W., Wang W., Wang S
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                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                            Gaps
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                                                                                                                                                      37.3%; Score 44; DB 10; Length 227; 38.1%; Pred. No. 21;
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Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SWART; SM00402; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS0066; MADS_BOX_2; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SEQUENCE 227 AA; 26401 MW; FEFF88A9AZAD7FEC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                         288 AA
                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                 1 NSPDSCEQQARNVQHYHKNEL 21
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 38.1.
best Local 8; Conservative
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SEQUENCE FROM N.A.
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CG18853.
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NCBI_TaxID=6239;
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL. AE003839.11; -
FLYBase; FEBGH0042173; CG18853.
InterPro; IPR000474; DNA_photolyase.
InterPro; IPR000288; DNA_photolyase_2.
Fram: PF00875; DNA_photolyase_2;
From: PF00875; DNA_photolyase_2;
SEQUENCE 288 AA; 33375 MW; 3682D8EBB635DDD4 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
W08D2.6 PROTEIN
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2
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Pred. No. 26;
6; Mismatches
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Pred. No. 32;
1; Mismatches
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32;
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Best Local Similarity 33.3%;
Matches 7; Conservative (
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ilarity 72.7%;
Conservative 1
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Best Local Similarity
Matches 8; Conserv
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Q23222
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417 AA

PRELIMINARY;

Created) PRT;

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STRAIN-ATCC27840;
Vannuffel P., Heusterspreute M., Bouyer M., Philippe M., Gala J.-L.;
"Molecular characterization of femA from Staphylococcus hominis,
Staphylococcus saprophyticus and Staphylococcus haemolyticus and femA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003447; FemAB.
Pfam; PF02388; FemAB; 1.
SEQUENCE 417 AA; 49034 MW; C5B6F1BF30B62009 CRC64;
                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FACTOR ESSENTIAL FOR METHICILLIN RESISTANCE FEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 based discrimination of staphylococcal species.";
Res. Microbiol. 0:0-0(1998).
EMBL; AF099964; AAC69633.1; -.
                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 35.2

11: Conservative
                                                                                                                                                                                                                                                Staphylococcus capitis.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=29388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Addms M.D., Celniker S.E., Lip'W. Fowns C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Manil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Barlew R.M., Basu A. Baxendall J., Bayraktarogul L., Benseley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
RA Burtis K.C., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Borson K., Doup L.E., Downes M., Dupgan-Rocha S., Dunkov B.C., Dunn P.,
RA Boston E., Gorgell J.H., Gu Z., Guan P., Heursk M.,
RA Hostin D., Harvey D., Heinan T.J., Hernandez J.R., Houck J.
RA Hostin D., Houston K.A., Heinand T.J., Hernandez J.R., Houck J.
RA Hostin D., Houston K.A., Hennandez J.R., Houck J.
RA Lasko P., Lei Y., Leviteky A.A., J. J., Li Z., Guan P., Mashreil A.,
RA Merkillov G., Milshina N.V. Modbary C., Mazny D.M., Nelson D.L.,
RA Lasko P., Lei Y., Morincoh T.C., McLeed M.P., Moshreil A.,
RA Hoston D.R., Noy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Ranigton K.A., Nixon K.A., Nixon K., Nussern D.,
Ra Remet R., Reinigton K., Saunders R., Wend S., Pent H.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
RA Hong Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ra Hang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
Ra Hang Z.-Y. Wassarman 
                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                           Last sequence update)
Last annotation update)
                                            412 AA.
                                                                                               Created)
                                         PRT;
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                                                          09v325;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD006705; UPF0066; 1
                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003839; AAF59182
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                                                                                                                                                                  CG12822 PROTEIN.
CG12822.
                                                                                                                                                                                                                                                                                                     Ephydroidea; Dro
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
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                                 Q9V325
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Gaps

10;

6; Indels

Length 417;

Score 44; DB 2;

37.3%;

Pred. No. 36; 4; Mismatches

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GENOMIC DNA, CHROWOSOME 5, P1 CLONE:MQN23.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryoct; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thallana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones.";
DNA Res. 5:203-216(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 44; DB 10; Length 439; 41.2%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AB013395, BAB11654.1; -.
SEQUENCE 439 AA; 48708 MW; 0058A0EFD9CFC31E CRC64;
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                                                                                                                                                  439 AA.
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281 NKRDNLQQQLDANQQKIDEAKNLQQEHGNEL 311
                                                                                                                                            PRT;
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MEDLINE-98403884; PubMed-9734815;
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                                                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                          Q9FJP7
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Gaps

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Score 44; DB 5; Length 412; Pred. No. 36; 6; Mismatches 8; Indels

37.3%;

1 NSPDSCEQOARNVOHYHKNEL 21 | :: || ||:|| :: 15 | 15 NEINNLRQOVRNLQHVQRKDI 35

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7; Conservative

Best Local Similarity
Matches 7; Conserv

Query Match

27

us-09-462-625-2_copy_55_75.rspt

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13,12
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50.0%;
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                                                                                              Ouery Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                  2 SPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                            Y49E10.23 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                         Barlow K.;
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081491;
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081491
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09XTT2
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                                                                                                                                                                                                                                    EMBO J. 13:6143-6151(1994).

-I- FUNCTION: THIS ENZYME CATALYZES THE LIGHT-DEPENDENT MONOMERIZATION (300-600 NM) OF CYCLOBOTYL PYRIMIDINE DIMERS (IN CIS-SYN CONFIGURATION), WHICH ARE FORMED BETWEEN ADJACENT BASES ON THE SAME DNA STRAND, UPON EXPOSURE TO ULTRAVIOLET RADIATION.
                                                                                                                                                                                                                 "A new class of DNA photolyases present in various organisms including aplacental mammals.";
                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-95112825; PubMed-7813451;
Yasui A., Eker A.P., Yasuhira S., Yajima H., Kobayashi T., Takao M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
NCBI_TaxID-5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L., McDonagh P., Stuart K.;
                                                                                                                                                                                                                                                                                                           RESIDUES (IN DNA).
--- COFACTOR: FAD (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE DNA PHOTOLYASE CLASS-2 FAMILY.
--- CAUTION: IT IS UNCERFAIN WHEFHER MET-1, MET-86 OR MET-106 IS
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D26021; BAA05042.1; -
FlyBase; F9gn0003082; phr.
InterPro; IPR000474; DNA_photolyase.
InterPro; IPR000208; DNA_photolyase_2.
Pfam; PF00875; DNA_photolyase_2.
ProDom; P000771; DNA_photolyase_2; 1.
PROSITE; PS01083; DNA_PHOTOLYASES_2_1; 1.
PROSITE; PS01084; DNA_PHOTOLYASES_2_2; 1.
Lyase: Chromophore; Flavoprotein; FAD; DNA repair; DNA-binding.
SEQUENCE 640 AA; 73819 WW; 388205226508871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DEOXYRIBODIPYRIMIDIE PHOTOLYASE (EC 4.1.99.3) (DNA PHOTOLYASE)
(PHOTOREACTIVATING ENZYME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
54:
     640 AA.
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     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 7; Conserv
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Q24443
Q24443;
01-NOV-1996 (
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Barsons J., Floyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                        Cawthra J., Handley F., Vogt C., Robertson L.,
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                                                                                                                                                                                                                             Length 701;
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Myler P.J., Sisk E., Cawthra J., Hanuly ...,
McDonagh P., Stuart K., Ivens A., Worthey E.A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC01016; AAG34192.1;
EMBL, AC018661; AAG22269.1;
EMBL, AC018661; AAG22269.1;
EMBL, AC018661; AAG22269.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
EMBL; 298866; CAB11567.1; -.
SEQUENCE 734 AA; 84685 MW; BC684D9EB00D3A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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13, Last sequence update)
17, Last annotation update)
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59;
                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                                                             Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44;
Pred. No.
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                           195 SPFSCSDSAKDVQEEHTASL 214
                                                                                                                                                                                                                          37.3%;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
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cunalyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Arabidopsis thaliana BAC F2401 from chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                       37.3%; Score 44; DB 10; Length 772;
46.7%; Pred. No. 65;
1ve 4; Mismatches 4; Indels
                                                        SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Murray J., Langston Y., Ahrens C.;
"The Sequence of A. thaliana F9D12.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              "The A. thaliana Genome Sequencing Project.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       Waterston R.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                           (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                    772 AA; 84873 MW; F5EDC2E5249A3206 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   778 AA.
                                                                                                                                                                                                                                                                                                       EMBL; AF077407; AAC26247.2; -.
InterPro; IPR000644; CBS.
InterPro; IPR001807; Volt_Cl_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00571; CBS; 2. Pfam; PF00571; CBS; 2. Pfam; PF00054; voltage_CLC; 1. PRINTS; PR00762; CLCHANNEL. SWART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 46.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| |: |||::|
654 HSPLPCDPSARNIRH 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSPDSCEQQARNVQH 15
                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                       STRAIN=CV. COLUMBIA;
Waterston R.;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.;
                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Q9MAV5
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Con L., Conway A. Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, RAC001113, RAF70851.1;
InterPro: IPR003864; DUF221.

SEQUENCE 778 AA, 89308 MW; 52533674565B3E95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE-97126010; PubMed-8969232;
Hechenberger M., Schwappach B., Fischer W.N., Frommer W.B.,
Jentsch T.J., Steinmeyer K.;
"A family of putative chloride channels from Arabidopsis and
functional complementation of a yeast strain with a CLC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.3%; Score 44; DB 10; 34.3%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 PDSDESISENVQHFFLVNHPDHYLTHQVVYNANEL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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P92943;
01-WAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87047 MW;
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Submitted (JAN-1998)
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Matches 12; Conserv
SEQUENCE FROM N.A.
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Length 792;

DB 10;

Score 44;

37.3%;

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Pfam; PF00072; response_reg; 1.
Pfam; PF00512; signal; 1.
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SM00388; HiskA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00344; BCTRLSENSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.3%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02518; HATPase_c; 1
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Best Local Similarity 29.4
Matches 10; Conservative
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Kinase; Phosphorylat
SEQUENCE 1057 AA;
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                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
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Q9C5T9
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                        Gaps
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EMBL: D64005; BAA10744.1; -.
HSSP; P04191; 1EUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suginra M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96127529; PubMed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
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                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9FD23;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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58.8%; Pred. No. 78;
tive 2; Mismatches
                                                                                                                                                                                                             945 AA.
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                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00119; CATATPASE.
PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
Pred. No.
                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                             PRT;
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InterPro; IPR001454; Hydrolase.
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Creat 01-NOV-1996 (TrEMBLrel. 01, Last 01-JUN-2001 (TrEMBLrel. 17, Last CATION-TRANSPORTING ATPASE PACL. PACL OR SLL0672.
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46.78;
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 58.8
hes 10; Conservative
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654 HSPLPCDPSARNIRH 668
                                                                                                                                                                                                             PRELIMINARY;
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                                                             1 NSPDSCEQQARNVQH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1148;
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Best Local Si
Matches 10;
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                                                                                                                                                                RESULT 33
059999
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                 Matches
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The Arabidopsis root.";

of the Arabidopsis root.";

dense Dev. 14:2938-293(2000)

Conserved two component hybrid molecule regulates the vascular pattern of the Arabidopsis root.";

dense Dev. 14:2938-293(2000)

Conserved two components of Sensory Transbuction Systems.

REGULATORY COMPONENTS OF SENSORY TRANSBUCTION SYSTEMS.

REMBL; AJ278530; CAC18523.1; ---

REMBL; AJ278529; CAC18521.1; ---

REMBL; AJ278529; CAC18529.1; ---

REMBL; AJ278529; CA
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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INOUE T., HJQUChI M., Hashimoto Y., Seki M., Kobayashi M., Kato T.,
SINODZAKI K., Kakimoto T.;
"Identification of a cytokinin receptor, CREI, from Arabidopsis.";
Submitted (OCT-2000) to the EMBL/Genbank/DBBJ databases.
-1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                        Pubwed-11114883;
Mahonen A., Bonke M.A., Kauppinen L., Riikonen M., Benfey P.N.,
Helariutta Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation; Receptor; Sensory transduction. 1057 AA; 117954 MW; E1381C8685F0D787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYTOXININ RECEPPOR CREIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB pred. No. 87; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HYHKN 19
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InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR001594; Harbase_c.
InterPro; IPR001561; His kina.
InterPro; IPR001789; Response_reg.
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CENTRAIN—CV. WASSILENSKIJA;

RC STRAIN—CV. WASSILENSKIJA;

RIOOUE T., Highundia M., Hashimoto Y., Seki M., Kobayashi M., Kato T.,

Satoshi T., Shinozaki K., Kakimoto T.;

Satoshi T., Shinozaki K., Kakimoto T.;

Tidentification of a cytokinin receptor, CRE1, from Arabidopsis.";

Submitted (OCT—2000) to the EMBL/GenBank/DDBJ databases.

LI-SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

RINGEPRO; IPRO003594; HAPPASS—C.

RINGEPRO; IPRO03561; His_kinA.

RINGEPRO; IPRO01789; Response—reg.
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.4%; Score 43; DB 10; Length 139; 66.7%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor; Sensory transduction.
AA; 120670 MW; 59496F734B528114 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2S ALBUMIN STORAGE PROTEIN.
2S ALBUMIN STORAGE PROTEIN.
43ACF35FE97D19B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galau G.A., Wang H.Y.C., Hughes D.W.;
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M83301; AAA33049.1; -.
Mendel; 14688; Goshi;2374;14688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
2S ALBUMIN STORAGE PROTEIN PRECURSOR.
MATS-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.3%; Score 44; DB 29.4%; Pred. No. 89; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEQOARNVQ-----HYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR001768; Cereal_tryp_amyl_inh.
InterPro, IPR003612; AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00234; tryp_alpha_amyl; 1.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02518; HATPase_c; 1.
Pfam; PF0072; response_reg; 1.
Pfam; PF00612; signal; 1.
PRINTS; PF00344; BCTRLSENSOR.
SMART; SM00387; HATPASE_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 AA; 15831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 29.4 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; Rec
SEQUENCE 1080 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 DSCEQQARNVQH 15
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                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                         Gaps
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel family of sensor histidine kinase genes in Arabidopsis thaliana.";
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                                                                                                                                     Score 44; DB 10; Length 1057;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.3%; Score 44; DB 10; Length 1080;
29.4%; Pred. No. 89;
tive 3; Mismatches 1; Indels 2
                                       Phosphorylation; Receptor; Sensory transduction.
SEQUENCE 1057 AA; 117894 MW; E121A86345F0C292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Sensory transduction.
1080 AA; 120730 MW; 5950DB968B529401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                    PRT; 1080 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                              -----HXHKN 19
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InterPro: IPR003594; HATPASSE_C.
InterPro: IPR003661; His_kinA.
InterPro: IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03518; HATPase_c; 1.
Pfam; PF0072; response_reg; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATPase_c; 1.
                                                                                                                                 37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB046871; BAB40776.1;
SMART; SM00388; H1SKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00388; HISKA; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                             10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.3
Best Local Similarity 29.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                       SM00448; REC; 1
                                                                                                                                                                                                                       6 CEQQARNVQ-----
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                                                                                                                              Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTIDINE KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jeguchi C.;
"A novel fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinase; P)
SEQUENCE
                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                Q9C5U0
                                                                                                                                                                                                                                                                                                                                   RESULT 36
Q9C5U0
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SWR
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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:109621; Alrp.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: |: |: |:|
214 TPEVIEKSVRDVEHWH 229
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SPDSCEQQARNVQHYH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| |:: | |
144 NSPDVCDEYKRTALH 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NSPDSCEQQARNVQH 15
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                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                       Query Match
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Ruchl P., Lewis S., Matsuo Y., Nikaido I., Peecole G., Quackenbush J.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Peecole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
Balake J., Bolidaya N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Pred. No. 23;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                     Created)
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STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Creat
01-NOV-1998 (TrEMBLrel. 08, Last
01-JUN-2001 (TrEMBLrel. 17, Last
KINFTOCHORE (SKP1P)-LIKE PROTEIN.
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Best Local Similarity 47.6
Matches 10; Conservative
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111111 | 1
34 DSCEQQIRKQAH 45
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MEDLINE=97195688; PubMed=9043061;
Zou Y., Evans S., Chen J., Kuo H.C., Harvey R.P., Chien K.R.;
"CARP, a cardiac anyrin repeat protein, is downstream in the Nkx2-5
                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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36.4%; Score 43; DB 11; Length 319;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                       36.4%; Score 43; DB 11; Length 266; 37.5%; Pred. No. 35; tive 6; Mismatches 4; Indels
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Schoenfeld J.R., Lowe D.G., Zou Y., Chen J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF041847, AACO35331;
EMBL; AF041849; AAB9708011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J., Chien K.R.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
Nature 409:685-690(2001).
EMBL, AKO06856; BAB24766.1.
MGD; MGI:1920656; 1700061405R1k.
SEQUENCE 266 AA; 30227 MW; 72788236776163F0 CRC64;
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PS50297; ANK REP_REGION; 1.
319 AA; 35939 MW; 6849DE07FD80517B CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CARDIAC ANKYRIN REPEAT PROTEIN MCARP.
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Development 124:793-804(1997).
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055014;
01-JUN-1998 (TIEMBLIEL 06,
01-JUN-1998 (TIEMBLIEL 06,
01-JUN-2001 (TIEMBLIEL 17,
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KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Rabito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruonstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Ruonstein M.J., Bult C., Fletcher C., Fullica M., Gariboldi M.,

Ruschincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ryachone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ryachia H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ryachia H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ryachia H., Ryachida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                          Jeyaseelan R., Poizat C., Abdishoo S., Kedes L.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U50736; AAD10401.1; -.
HSSP; Q00421; IAWC.
InterPro; IFR002110; ANK.
Pfam; PF00023; ank; 4.
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Last annotation update)
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319 AA
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PROSITE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 319 AA; 36075 MW; F78EE
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                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY;
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Matches 7; Conserv
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                                                       01-MAY-1999
01-MAY-1999
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Q921F0
Q921F0;
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Jones R.M., Collier L.S., Neidle E.L., Williams P.A.; "areABC genes determine the catabolism of aryl esters in Acinetobacter
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MEDLINE-94150718; PubMed-7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_raxID=6239;
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                                                                                                                   Length 319;
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                                                                                                                                            Indels
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MGD; MGI:109621; Alrp.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 4.
PROSITE; PS50088; ANK_REPEAT; 4.
SROUBNCE 319 AA, 36003 MW; 26A3C4062CF0E7D0 CRC64;
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR002168; Lipolytic_arayme
PROSITE; PS01174; LIPASE_GDXG_SER; UNKNOWN_1
SEQUENCE 326 AA; 37066 WW; FF00B3549864AA57 CRC64;
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Last annotation update)
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                                                                                                                  Score 43; DB Pred. No. 41;
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46.7%;
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01-FBB-1997 (TrEMBLrel. 02,
01-FBE-1997 (TrEMBLrel. 02,
01-NOY-1998 (TrEMBLrel. 08,
COSMID F57F4.
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                                                                                                    Query Match
Best Local Similarity 46.'",
-has 7; Conservative
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Best Local Similarity 50.00.
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J. Bacteriol. 0:0-0(1999).
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144 NSPDVCDEYKRTALH 158
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Caenorhabditis elegans
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Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas R., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
sperMIDINE/PUTRESCINE ABC TRANSPORTER, ATP-BINDING PROTEIN (POTA).
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36.4%; Score 43; DB 5; Length 327;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2: Indels
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Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           Miller N., Bradshaw H.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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39580 MW; 5EA65C9F8BC04DAA CRC64;
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Bacteria: Spirochaetales; Spirochaetaceae; Borrella.
NCBL_TaxID=139;
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam: PF00005; ABC_tran; 1.
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STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
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TIGR; BB0642; -.
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Nature 368:32-38(1994).
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201 RKAASVAHYHKN 212
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                       Gaps
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NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                 "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
RMEL; AL338994; CAC22689.1; --
Hypothetical protein.
SEQUENCE. 353 Aa; 39520 MW; 07DID1961DE69A77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 353;
Length 347;
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                         Indels
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Last sequence update)
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Viruses; dSDNA viruses, no RNA stage; Asfarviridae;
African swine fever-like viruses.
                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 39.5 KDA PROTEIN.
12743.08.
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 DB 2;
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                         Mismatches
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 Score 43;
Pred. No.
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 36.4%;
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Best Local Similarity 47.1-
Best Local Similarity 47.1-
Best Local Similarity
Conservative
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  Query Match 36.4
Best Local Similarity 37.5
Matches 6; Conservative
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                                                  4 DSCEQQARNVQHYHKN 19
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Eukaryota; Euglen
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Q65153;
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Q65153
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polymerases.";
Nucleic Acids Res. 21:2423-2427(1993).
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                                                                                      PubMed=8506138;
                                                                                                                                                                                       MEDLINE-93353606; PubMed-8102411;
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MEDLINE-93327788; PubMed-8335009;
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MEDLINE-92260660; PubMed-1583732;
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                                                                                      MEDLINE-93281390;
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        Camacho A., Vinuela E.;
"Protein p22 of African swine fever virus: an early structural protein
that is incorporated into the membrane of infected cells.";
Virology 181:251-257(1991)
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*African swine fever virus thymidylate kinase gene: sequence and
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Blasco R., Lopez-Otin C., Munoz M., Bockamp E.O., Simon-Mateo C.,
                                                                                                                                      Gonzalez A., Calvo V., Almazan F., Almendral J.M., Ramirez J.C., La Vega I., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: family 360.";
                                                                                                                                                                                                                  MEDLINE-90219204; PubMed-2325202;
Almendral J.M., Almazan F., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: family 110.";
J. Virol. 64:2064-2072(1990).
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                                             La Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.; "Nucleotide sequence and variability of the inverted terminal repetitions of African swine fever virus DNA."; Virology 201:152-156(1994).
                                 MEDLINE=94233765; PubMed=8178480;
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MEDLINE-94065656; PubMed-8245848;
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J. Gen. Virol. 74:1633-1638(1993)
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Vinuela E.; "Sequence and evolutionary relationships of African swine fever virus thymidine kinase."; Virology 178:301-304(1990).
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MEDLINE-9333210; PubMed-8474154;
MEDLINE-9333210; PubMed-8474154;
MEDLINE-9333210; PubMed-8474154;

"Sequence and characterization of the major early phosphoprotein p32 of African swine fever virus.";
J. Virol. 67:2475-2485(1993).
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MEDLINE=90223993; PubMed=2327074;
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"Mapping and sequence of the gene coding for protein p72, the major capaid protein of African swine fever virus.";
Virology 175:477-484(1990).
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EMBO J. 12:2977-2987(1993).
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Virology 188:938-947(1992).
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of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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*Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
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"African swine fever virus guanylyltransferase.";
Virology 193:319-328(1993).
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
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                                 Yanez R.J., Vinuela E.;
"African swine fever virus encodes a DNA ligase.";
Virology 193:531-536(1993).
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MEDLINE-93188700; PubMed-8446027;
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              MEDLINE-93174976; PubMed-8438592;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatides P.G., Scherer S.E., I.P.W., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
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RA Abril J.F., Apdraws-Pfannach. P., Balawin D.,
RA Abril J.F., Apdrawal A., An H.-J., Andraws-Pfannach. P., Balawin D.,
RA Ballew R.W., Basu A. Baxendla G., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Deng E.., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.W., Cawley S., Dahlke C., Rerraz C., Ferraz C., Ferraz C.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Renrison D.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C.,
Gabriellan A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
ROSIer C., Gabriellan A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J. R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Malbiha N.V., Mobarry C., Mories J., Moshrefi A.,
Rosko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Li X.,
Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Li X.,
Rollen Kiamos I., Shapon M., Stropki M.P., Shue B.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Staplecton M., Stropki M., Welssen M.,
Whong Y., Wasserman D.A., Welson D.A.,
Wang Z.-Y.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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InterPro; PR001478; PD2.
InterPro; IPR001478; PD2.
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Pfam; PR00089; trypsin; 1.
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SEQUENCE 452 AA; 45129 MW; 6CA675EB0911F983 CRC64;
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
DR EMBL; AE003830; AAF58812.1;
DR FlyBase; FBG0028426; JhI-1.
SQ SEQUENCE 743 AA; 82895 MW; 704327777345D0ID CRC64;
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Query Match 36.4%; Score 43; DB 5; Length 743; Best Local Similarity 46.7%; Pred. No. 91; Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps

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Qy 4 DSCEQQARNVQHYHK 18 |: | ::|1|||| Db 693 DNMEVTVEDLQHYHK 707 Search completed: December 17, 2001, 07:51:42 Job time: 124 sec

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Oce version 4.5	3 - 2000 C	ing sw model	2001, 07:50:03; Search time 10.21 Seconds (without alignments) 75.412 Million cell updates/sec	PX_55_75 HKNEL 21	Gapext 0.5	6664827 residues	chosen parameters: 100059	0	0% 100% 150 summaries		results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution	SUMMARIES	ID Description	TBX8_CAEEL Q22292 caenorhabdi D7_DICDI DFFA_ANTMA P23706 antirrhinm	Q01076 P33945	09zka2 P56468		006443	P87000	P76117	P13800 Q50724	049736 002740	P56698	007472	P/0460			P35736 P37775	P4823 some supre P4823 saccharomy	P37
	cencor Copyright (c) 1993	protein - protein search, usi	Run on: December 17, 2	title: US-09-462-625-2_CO Perfect score: 118 Sequence: 1 NSPDSCEQQARNVQHY	coring table: BLOSUM62 Gapop 10.0 , G	earched: 100059 seqs, 3	Total number of hits satisfying	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 1 Maximum Match 1 Listing first 1	t_39:*	Pred. No. is the number of r score greater than or equal and is derived by analysis c		Result Query No. Score Match Length DB	1 342 1 1 850 1 3 227 1	44 37.3 471 1 43 36.4 360 1 43 36.4 360 1	43 36.4 440 1 43 36.4 440 1	42.5 36.0 1140 1 42 35.6 253 1	42 35.6 357 1 42 35.6 503 1	42 35.6 865 1 41.5 35.2 321 1	41 34.7 205 1	41 34.7 786 1	41 34.7 1103 1	41 34.7 2326 1 40.5 34.3 450 1	40 33.9 231 1 40 33.9 376 1	40 33.9 432 1	40 33.9 507 1	40 33.9 881 1	40 33.9 922 1 40 33.9 1124 1	40 33.9 1178 1 39.5 33.5 1472 1	39 33.1 148 1

067367 aquifex aeo 012403 saccharomyc 001170 chlorella v P48569 saccharomyc 089100 m grb2-rela P56705 hom osapien P22724 mus muschilus gall 094275 hom osapien P51030 gallus gall 042122 oryzias lat p35950 saccharomyc 094666 schizosacch P28363 saccharomyc p28716 euplotes oc P53951 mycobacteri p97874 rattus norv P28716 euplotes oc P63951 mycobacteri p97874 rattus norv P68041 fremyella d 084275 chlamydla t 099604 caenorhabdi P78820 saccharomyc P63953 saccharomyc P63951 mus musculu P55108 mattus norv P1410 pichia jadi periodo sapien P53063 saccharomyc P53063 saccharomyc P53064 saccharomyc P53064 saccharomyc P53064 saccharomyc P53064 saccharomyc P53064 saccharomyc P53064 saccharomyc P5510 mycoplasma P53064 saccharomyc P5510 mycoplasma P53064 saccharomyc P5510 mycoplasma P53064 saccharomyc P5510 mycoccus P55249 human herpe P65249 human herpe P65249 human herpe P653947 saccharomyc P55107 drosophila O95177 drosophila P16653 adulitex aeo 003249 mus musculu P25347 saccharomyc P55107 homo sapien P5

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Rhabditidae; Peloderinae; Caenorhabditis.
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P46347
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P18723
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Q62925
Q13233
P31352
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Q13315
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09upn3
P46690
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P35945
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P97884
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ATM_HUMAN
ACF7_MOUSE
                                                                                                                                                                                                                                                                                     SIX2_MOUSE
VV_RINDR
                                                                                                                                                        TCF8_CHICK
YKT3_CAEEL
M3K1_RAT
                                                                                                                                                                                                                                                 GAS4_ARATH
Y082_RICPR
YDE2_SCHPO
                                                                                                                                                                                                                                                                                                                                                           CERU_RAT
A4E1_HUMAN
                                                                            2G48_XENLA
CFAB_MOUSE
ZW10_HUMAN
                                                                                                          E2F_DROME
LDLR_MOUSE
Y304_TREPA
                                                                                                                                                                                       M3K1_HUMAN
RRPL_MABVM
                                     DRTS_PLAVI
IPAA_SHIFL
HS74_ANOAL
YB65_SCHPO
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          Y514_SYNY3
YM44_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                            CKCB_PASHA
                             RBJK_DROME
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                                                                                                                                                                                                                                                                                                                                                 VL96_IRV1
                                                                                                                                                                                                                                                                                                                                                                                       713K_SSV1
                                                                                                                                                 CF8_RAT
                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
Durbin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2
NCBI_TaxID=6239;
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TBX8_CAEEL
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CAMP-INDUCIBLE PRESPORE PROTEIN D7.
POLY-GLN.
POLY-ASN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-BOX.
: 926DA46941277C49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetczoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1;
Pred. No. 8.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DT_DICDI STANDARD; PRT; 850 AA. ID D7_DICDI STANDARD; PRT; 850 AA. ID D7_DICDI STANDARD; PRT; 850 AA. ID D7_OCT-1996 (Rel. 34, Last sequence update) DT 01-0CT-1996 (Rel. 35, Last annotation update) DT 01-0VJ-1997 (Rel. 35, Last annotation update) DE CAMP-INDUCIBLE PRESPORE PROTEIN D7 PRECURSOR.
SIMILARITY: CONTAINS A T-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AX3;
MEDLINE=95080502; PubMed=7988791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 AA; 38923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ar protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U25143; AAA73514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.1%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01283; TB0X_1; 1.
PROSITE; PS01264; TB0X_2; 1.
PROSITE; PS50252; TB0X_3; 1.
DNA-binding; Nuclear protein
                                                                                                                                                                                                                                          EMBL; 229443; CAA82578.1; -.
HSSP; P24781; 1XBR.
                                                                                                                                                                                                                                                                                     WormPep; TOTC4.12; CE21157.
InterPro: IPR001699; T-box.
DRAIN; PR00907; T-box; 1.
PRINTS; PR00907; TBOX.
SWART; SM00425; TBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
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18 NLFHYHKNEM 27
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Pfam; PF00319; SRF-TF; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                          Antirrhinum majus (Garden snapdragon).

Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bormatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.

NCBI_TaxID=4151;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=90183955; PubMed=1968830;
Sommer H., Beltran J.-P., Huijser P., Pape H., Loennig W.-E.,
Saedler H., Schwarz-Sommer Z.;
"Deficiens, a homeotic gene involved in the control of flower
morphogenesis in Antirrhinum majus: the protein shows homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
                                                            .;
0
                                        Score 45; DB 1; Length 850;
Pred. No. 23;
                                                            4; Indels
 728 738 POLY-GLN.
850 AA; 95343 MW; 13BA634CCE7AA502 CRC64;
                                                                                                                                                           01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                              227 AA.
                                                         3; Mismatches
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                                                                                                                                              PRT;
                                                                                                                                                                                         FLORAL HOMEOTIC PROTEIN DEFICIENS.
                                                                                                                                                                                                                                                                                                                                                                STRAIN=SIPPE50;
MEDLINE=92155166; PubMed=1346760;
                                     38.1%;
50.0%;
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InterPro; IPR002100; MADS-box.
Pfam; PF01486; K-box; 1.
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                                                       7; Conservative
                                                                                                                                             STANDARD;
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                                                                                    ||| : | :|||
810 SPDQIKNQLKNIQH 823
                                                                         2 SPDSCEQQARNVQH 15
                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                          DEFA_ANTMA P23706;
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      Gaps
PRINTS; PR004(4; MADSDOMIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
Transcription regulation; DNA-binding; Activator; Nuclear protein; Developmental protein.
DOMAIN 93 165 K-BOX.
SEQUENCE 227 AA; 26279 MW; 95E3FF60924FDE8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDIINE-93219140; PubMed-8464750;
Adhikari P., Berget P.B.;
"Sequence of a DNA injection gene from Salmonella typhimurium phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterlophage P22.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
NCBI_TaxID=10754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kropinski A.M.B., VanderByl C.S., "The completed sequence of genome of Salmonella phage P22."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                             37.3%; Score 44; DB 1; Length 227; 36.8%; Pred. No. 8.3; Live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AA; 50100 MW; EA6366D094D10A9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA FRANSFER PROFEIN GP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 21:1499-1499(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF217253; AAF75054.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               145 NQIDTSKKKVRNVEEIHRN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L07556; AAA62407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                1 NSPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 36.88
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M93985; AAA72116.1;
PIR; D43330; D43330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VG20_BPP22
Q01076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
VG20_BPP22
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Length 471;

Score 44; DB 1; Pred. No. 18;

37.3%; 36.8%;

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185 NFPKGSEEQARSLMNLONNE 204
                   1 NSPDSCEQQARNVQHYHKNE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuiken G.A., Bertens P.J.A., Peterson-Maduro J., Veenstra G.J.C.,
Koster J.G., Destree O.H.J.;
"The promoter of the Xwnt-5C gene contains octamer and AP-2 motifs
functional in Xenopus embryos.";
Nucleic Acids Res. 22:1675-1680(1994).
-!- PRUKTION: PROBABLE DEVELOPMENTAL PROTEIN: MAY BE A SIGNALING
MOLECULE MHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
-!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00110; wnt; 1.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
SIGNAL

1 1 6 POTENTIAL.
CHAIN

17 360 WNT-5C PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - DEVELOPMENTAL STAGE: EXPRESSION IN THE EARLY GASTRULA STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Stegeman B., Peterson J., Eizema Stabel L., Dekker E.J., Destre O.H.J.; Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; Length 360;
Pred. No. 19;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S -> C (IN REF. 2).
93CBD15D7A92779E CRC64;
                                                                                                                                                                                                          WNSC_XENLA STANDARD; PRT; 360 AA. P33945; 091928; 01-FEB-1994 (Rel. 28, Created) PFEB-1994 (Rel. 28, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update)
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·!- SIMILARITY: BELONGS TO THE WNT FAMILY
                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                             WNT-5C PROTEIN PRECURSOR (XWNT-5C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94261437; PubMed-8202371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΜW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X73510; CAA51916.1; -. EMBL; X76190; CAA53784.1; -. PIR; S34173; S34173.
                                                                        :||:::| |:| | 411 SSPEAMQOSIREIQEYTUN 429
                                            1 NSPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000970; Wntl.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                      WN5C_XENLA
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)
-5-AMINOIMIDAZOLE = FUMARATE + 5'-PHOSPHORIBOSYL-5-AMINO-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PATHWAY: EIGHT STEP IN DE NOVO PURINE BIOSYNTHESIS.
-1- SIMILARITY: BELONGS TO THE LYASE I FAMILY. ADENYLOSSUCINATE LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 43; DB 1; Length 440; 41.2%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACID (BY SIMILARITY).
BASE (BY SIMILARITY).
C67D3C02AEFA2EFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001531; AAD06609.1; -.
InterPro; IPR000362; Fumarate_lyase.
Pfan; PF00206; Iyase_1; 1.
PRINTS; PR00145; DCRYGTALI.N
PRINTS; PR00149; FUMRATELYASE.
PROSITE; PS00163; FUMRATE_LYASES; 1.
PUT.LIDE blosynthesis; Lyase; Complete proteome.
Put.Libe 68 ACID (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PURB_HELPY STANDARD; PRT; 440 AA P54068; Rel. 36, Created) 15-J0L-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 SCEKIAVNIRHLQRSEV 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.4
Best Local Similarity 41.2
Matches 7; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=85963;
                                                                                                                                                                                    PURB OR JHP1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY
                                                  30-MAY-2000 (
PUR8_HELPJ
09ZKA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARE
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Gaps

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8; Indels

4; Mismatches

Conservative

36.4%;

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us-09-462-625-2_copy_55_75.rsp

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943 AA;
                    SEQUENCE FROM N.A.
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                                 TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHJL OR B3530.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                          117141; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centromere.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHJL_ECOLI
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                                                                                                                                                                                                                                                                                              Nature 388:539-547(1997).
-1- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)
-1- S-AMINOIMIDAZOLE - FUNARATE + 5'-PHOSPHORIBOSYL-5-AMINO-4-
IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP -
                                                                                                                                             Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fulil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: EIGHT STEP IN DE NOVO PURINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE LYASE I FAMILY. ADENYLOSSUCINATE LYASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                      Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                        "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
20-AUG-2001 (Rel. 40, Last annotation update)
ADENYLOSUCCINATE LYASE (EC 4.3.2.2) (ADENYLOSUCCINASE) (ASL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGK; ...
InterPro. IPRUU....;

Pfam: PP00206; lyase_1; l.

R PRINTS; PR00149; FUMRATELYASE.

JA PROSITE; PS00163; FUMRATE_LYASES; l.

R PRINTS; PS00163; FUMRATE_LYASES; l.

PUTINE bioSynthesis; Lyase; Complete proteome.

"" SITE 66 68 ACID (BY SIMILARITY).

"" 11 141 BASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 1; Length 440; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                  MEDLINE-97394467; PubMed-9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENC_HUMAN STANDARD; E 003188; Q9P0M5; 01-0CT-1993 (Rel. 27, Created) 01-0CT-1993 (Rel. 27, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000617; AAD08156.1;
                                                                                                        SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 SCEKIAVNIRHLQRSEV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SCEQOARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                       FUMARATE + AMP).
                                                                               NCBI_TaxID=210;
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                         PURB OR HP1112
                                                                                                                                                                                                                                                                                                                                                                                              SUBFAMILY.
                                                                                                                                                                                                                                                          Venter J.C.
                                                                                                                                                                                                                                                                                     pylori.
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                                                                                                                                                                                                                                                                                                                                                           participation in cell cycle regulation in late G1-phase and expression control by E2F-1, pRD, p107 and Sp-1... Submitted (MAX-1999) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.; "Analysis of the Escherichia coll genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
1, 6DB0810A35476376 CRC64;
MEDLINE-92323541; PubMed-1339310;
Saitch H., Tomkiel J., Cooke C.A., Ratrie H. III, Maurer M.,
Rothfield N.F., Earnshaw W.C.;
"CENP-C, an autoantigen in scleroderma, is a component of the human
inner kinetochore plate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nuclear protein; DNA-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
                                                                                                                                                                                                                                                                                                                                 'Promoter characterization of centromere protein C reveals its
                                                                                                                                                                                                                             SEQUENCE OF 1-21 FROM N.A.
Poppe M., Botz J., Hahm B., Dobat K., Eickelbaum W., Paweletz
Arand M., Knehr M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YHJL_ECOLI STANDARD; PRT; 1140 AA.
P37650; P76710;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 128.7 KDA PROTEIN IN DCTA-DPPF INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NORMAL KINETOCHORE ASSEMBLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed~8041620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M95724; AAA51974.1; -. EMBL; AF151723; AAF73191.1; -.
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41.2%;
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129 NTPDSKKISSRNINDHH 145
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                                                                                                                                                                     Cell 70:115-125(1992).
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93315143; PubMed-7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97426617; PubMed-9278503;
Blattner F.K., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vided J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                            MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: STRONG, TO ACETOBACTER XYLINUM CELLULOSE SYNTHASE
OPERON PROTEIN C (ACSC/BCSC).
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Escherichia
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01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-NGG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 28.2 KDA PROTEIN IN TNAB-BGLB INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia col1 K-12."; Science 277:1453-1474(1997).
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Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000430; AAC76555.1; ALT_INIT.
EcoGene; EG12257; yhjL.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO 101-152.
                                        REVISIONS TO 577-578.
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                                                              MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
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NEARAQLITLR -> VNVASIWNYSVRRAGFIAHTRPITTP
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-!- DEVELOPMENTAL STAGE: UNDETECTABLE IN THE BLASTULA. APPEAR WITH
GASTRULATION, IS PRESENT THROUGHOUT NEURULATION AND ORGANGENESIS,
AND DECREASE TO BARELY DETECTABLE LEVELS IN HATCHED LARVAE.
-!- SIMILARITY: BELONGS TO THE WAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-i- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                               FPAMNRYGSVNKTILTKRGRAHHAA (IN REF. 1).
5A4418BF7CD73CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93183769; PubMed-8443107;
Busse U., Seguin C.;
"Isolation of cDNAs for two closely related members of the axolotl Wht family, Awnt-5A and Awnt-5B, and analysis of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 253,
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Pred. No. 19;
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(Rel. 29, Last sequence update)
(Rel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                     EMBL; AE000448; AAC76735.1; -. EcoGene; EG11722; yieE. EcoGene; EG11722; yieE. Expothetical protein; Complete proteome. CONFLCT 101 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 253 AA; 28191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambystoma mexicanum (Axolotl).
                                                                                                                                                                                                                                                                  EMBL; L10328; AAA62063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.6%;
35.3%;
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Mech. Dev. 40:63-72(1993).
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InterPro; IPR000970; Wntl.
Pfam; PF00110; wnt; 1.
SMART; SM00097; WNTl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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01-JUN-1994
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01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                               Gaps
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLYCOPROTEIN POLYPROTEIN PRECURSOR [CONTAINS: GLYCOPROTEINS G1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85033957; PubMed-6492264;
Mayorin D.D., Romanowski V., Galinski M., Bishop D.H.L.;
Sequencing studies of pichinde arenavirus S RNA indicate a novel coding strategy, an ambleense viral S RNA.";
J. Virol. 52:897-904 (1984).
                                                                                                                                               · · · ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pichinde arenavirus.
Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
NCBL_TaxID=11630;
                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                            Length 357;
                                                               POTENTIAL.
WNT-5B PROTEIN.
N'LINKED (GLCNAC. .) (POT'N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                          9; Indels
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                                                                                                                                                                                                                                                                                       Score 42; DB 1;
Pred. No. 27;
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PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-87160943; PubMed-2435460;
                                                                                                                                                                                                              40086 MW;
                                                                                                                                                                                                                                                                                35.6%;
40.0%;
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182 NYPKGSEEQARTLMNLQNNE 201
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                                                                                                                                                                                                                                                                                                                                  8; Conservative
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357 AA;
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Matches 8; Conserv
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P03540;
                                                                                     CHAIN
CARBOHYD
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VGLY_PTARV
VGLY_P
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-i- DOMAIN: THE GLUTAMINE-RICH DOMAIN MIGHT FUNCTION IN ACTIVATING
                                          GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
           (POTENTIAL)
                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENE EXPRESSION.
-!- SIMILARITY: CONTAINS 1 2N(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 865;
    N-LINKED (GLCNAC. . . ) (POT.
N-LINKED (GLCNAC. . . ) (POT.
N-LINKED (GLCNAC. . . ) (POT.
N-LINKED (GLCNAC. . ) (POT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=74A, ZTA, Bibbins M., Connerton I.F.; Bibbins M., Connerton I.F.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.-I- FUNCTION: POSITIVE REGULATOR OF ACETATE INDUCTION.-I- SUBCELLULAR INCAPTION. WITTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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865 AA; 96407 MW; A75499B2E9435C36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     AC15_MEUCR STANDARD; PRT; 865 AA.
AC P87000;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 11-NOV-1997 (Rel. 35, Last annotation update)
DT 11-NOV-1997 (Rel. 35, Last annotation update)
DT 11-NOV-1997 (Rel. 35, Last annotation update)
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Mismatches
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Pred. No.
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57278 R
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Best Local Similarity 40.0°
Matches 8; Conservative
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503 AA;
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Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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P13800;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Macyor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                       Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 23.3 KDA PROTEIN IN ANSP-RHSE INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.2%; Score 41.5; DB 1; Length 321; Best Local Similarity 34.6%; Pred. No. 29; Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                        MEDLINE-90287727; PubMed-2356131;
Seurinck J., Truettner J., Goldberg R.B.;
"The nucleotide sequence of an anther-specific gene.";
Nucleic Acids Res. 18:3403-3403(1990).
-I- TISSUE SPECIFICITY: ANTHER-SPECIFIC (TAPETAL CELLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLY.
POLY-GLY.
9FE4AFB33F2070BD CRC64;
                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
ANTHER-SPECIFIC PROTEIN TA-29.
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                                                                 PRT;
                                                                                                                                               Nicotiana tabacum (Common tobacco).
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EMBL; X52283; CAA36524.1; -.
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                                                                  STANDARD;
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STRAIN-K12 / MG1655;
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=4097;
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NCBI_TaxID=562;
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                                                                 TA29_TOBAC
P24804;
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01-FB1-1991 (Rel. 17, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
TRANGCRIPTIONAL REGULATORY PROTEIN DEGU (PROTEASE PRODUCTION ENHANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE-89933891; PubMed-3141378;
Henner D.J., Yang M., Ferrari E.;
Honer D.J., Zang M., Ferrari S.;
Hocalization of Bacillus subtilis sacU(Hy) mutations to two linked genes with similarities to the conserved procaryotic family of two-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINES B903890; PubMed=3141377;

Kunst F., Debarbouille M., Msadek T., Young M., Maueel C.,

Karamata D., Klier A., Rapoport G., Dedonder R.;

"Deduced polypeptides encoded by the Bacillus subtilis sacU locus
share homology with two-component sensor-regulator systems.";

J. Bacteriol. 170:5093-5101(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka T., Kawata M.; "Cloning and characterization of Bacillus subtilis lep, which has positive and negative effects on production of extracellular
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. BETA SUBFAMILY.
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein; Transferase; Complete proteome. 205 AA; 23321 MW; 8EC9279D071D2813 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1;
Pred. No. 22;
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J. Bacteriol. 170:5102-5109(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.78;
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118 APDAPEQLKKNVIEYRKS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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RESULT 18
YY01_MYCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnler T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
FUNCTION: REGULATING FACTOR FOR THE PRODUCTION OF EXTRACELLULAR PROTEASES. THE N-TERMINAL REGION ACTS AS AN INHIBITOR, WHEREAS THE C-TERMINAL REGION CARRIES BURANCING ACTIVITY.

SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIGEILLO, FENOLOGIC, COLEGE TO THE PROBLEM PROBLEM PROBLEM PROBORD TO THE PERMITS PROBORD TO THE THE LUXR.

PRINTS; PROBORD HTHE LUXR; 1.

SWART; SMO0418; REC; 1.

PROSITE; PSOB622; HTHE LUXR_FAMILY; 1.

Sensory transduction; Phosphorylation; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIF (BY SIMILARITY).
F059DC9237DC264A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 229;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Activator; Repressor; Complete proteome.
DOMAIN 1 101 RECEIVER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 87.3 KDB PROTEIN RV3401.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P10957; IRNL.
Subtilist; BG10393; degu.
InterPro; IPR000792; HTH_LuxR.
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                   EMBL, M21658; AAA22545.1; --
EMBL, M23558; AAA22733.1; --
EMBL, M2649; AAA22735.1; --
EMBL, A08709; CAA00807.1; --
EMBL, U56901; AAC44938.1; --
EMBL, 299122; CAB15566.1; --
PIR; C30191; RGBSXD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 AA; 25866 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.78;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 34.7
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 :: || |:|||
36 DDGDEAARIVEHYH 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                        REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YY01_MYCTU
ID YY01_MYCTU
AC Q50724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
DNA_BIND
SEQUENCE
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                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR-CDC 1551 / Oshkosh;
STRAIR-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Eiglmeier K., Parkhili J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M., Stutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 65 OF GLYCOSYL HYDROLASES. STRONG,
TO M.LEPRAE ML0392.
                                                                                                                                                                                                                                                                                                                                                                                                                        genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genomes sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculist, Rv3401; -.
Hypothetical protein; Hydrolase; Glycosidase; Complete proteome.
SEQUENCE 786 AA; 87315 MW; 73CB5E78DAD10AE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1; Length 786;
Pred. No. 89;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.R., Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001 (Rel. 35, Last sequence update)
HYPOTHETICAL 88.1 KDA PROTEIN ML0392.
MyCobacterium 1.20.Fl.30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     792 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21128732; PubMed-11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007156; AAK47846.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z77165; CAB01022.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 EQKARNVDYYER 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 EQQARNVQHYHK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT3509; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YY01_MYCLE
Q49736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole
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send an email to license@isb-sib.ch)
                                                                                                                                                                 Lyase; cGMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAB_DISOM
P56698;
                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                             ision.
                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAB_DISOM
                                                                                                                                                                                                                                                                                                                                                                   Matches
   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: THERE ARE 9 CONSERVED CYSTEINE RESIDUES IN SENSORY GUANYLATE CYCLASES, 6 IN THE EXTRACELLULAR DOMAIN, WHICH MAY BE INVOLVED IN INTRA- OR INTERCHAIN DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-1091 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
21. SETINAL GUANNILY CYCLASE 2 PRECURSOR (EC 4.6.1.2) (GUANYLATE CYCLASE 2F, RETINAL) (REGC-2) (GOOTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F).
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                TO M.TUBERCULOSIS RV3401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                al protein; Hydrolase; Glycosidase; Complete proteome. 792 AA; 88087 MW; DFAFCBECCA4E20C8 CRC64;
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                             Score 41; DB 1; Length 792;
Pred. No. 90;
                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
             "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                              PRT; 1103 AA
                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                              34.7%;
58.3%;
                                                                                                                                                              EMBL; U00015; AAC43240.1; -.
                                                                                                                                                                            EMBL; AL583918; CAC29900.1;
                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                           608 EQKARNVDYYER 619
                                                                                                                                                                                                                                                                                            7 EQQARNVQHYHK 18
                                                                                                                                                                                       Leproma; ML0392; -.
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUCY 2F OR GUCZF
Barrell B.G.;
                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                           CYGF_BOVIN
O02740;
                                                                                                                                                                                                              SECUENCE
                                                                                                                                                                                                                                                                                                                                                     KESULT 19
CYGF_BOVIN
                                                                                                                                                                                                                                                                     Matches
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COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM AND ACTIVITY. THE ANXILIARY SUBUNITS BETA AND ALPHA-2/DELTALINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Electric lobe;
MEDLINE-91248175; PubMed-7683405;
HOTHE W.A., Ellinor P.T., Imman I., Zhou M., Tsien R.W., Schwarz T.L.;
Molecular diversity of Ca2+ channel alpha 1 subunits from the marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discopyge ommata (Electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchi; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torppadiniformes; Narcinoidel; Narcinidae; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
PROBABLE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:3787-3791(1993).
-!- FUNCTION: THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM
CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLFAGE
ACTIVATED" (HVA) GROUP (BY SIMILARITY).
-!- SUBUNIT: VOLFAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
                                                                                                                                                                                                                                                                                                                                                   synthesis; Signal; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
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8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
MW, EB731E1D8C642A44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUANYLATE CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.36
2; Mismatches
                                                                                                                                                                                                                                                              PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1. PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                Interpro; IPR001828; ANF receptor.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR001054; Guanylt_cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                           1; guanylate_cyc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 SAASLVQHSRNVQFYGFNQL 393
                                                                                                                                         Pfam; PF01094; ANF_receptor;
Pfam; PF00211; guanylate_cyc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
EMBL; U95958; AAB53864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
SMART; SM00044; CYCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 50.0
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1103 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
452
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             ITSSUE SPECIFICITY: EXPRESSION IS HIGHER IN THE ELECTRIC LOBE THAN IN THE POREBRAIN.

DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBERANE SEGMENTS (51, 22, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (54). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00520; ion_trans; 4.
PRINTS; PR00167; CACHANNEL.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; REPEAT 75 351
                                                                                                                                                          SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S2 OF REPEAT I (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
S3 OF REPEAT I (POTENTIAL).
S4 OF REPEAT I (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
S5 OF REPEAT I (POTENTIAL).
S1 OF REPEAT I (POTENTIAL).
S2 OF REPEAT I (POTENTIAL).
S1 OF REPEAT II (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
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S7 OF REPEAT II (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
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S7 OF REPEAT III (POTENTIAL).
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S5 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
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S3 OF REPEAT III (POTENTIAL).
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S1 OF REPEAT I (POTENTIAL)
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                EMBL; L12532; -; NOT_ANNOTATED_CDS.
InterPro; IPR002077; Ca_channel.
InterPro; IPR00011; Cat_channel_TrpL.
InterPro; IPR000536; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR002048; EF-hand.
 ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00036; efhand; 1.
Pfam; PF00520; ion_trans;
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                                                                                                                                                                                       BINDIA HAS TO THE BETA SUBUNIT (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
PHOSPHORIAATION (BY CAPK) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                              D -> DDGLGIIYEPEQKPEDIQSVY (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AVONPORT;
Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                               PHOSTAL PROPERTY.

N-LINKED GLCNAC. . . (POTENTIAL).

N-LINKED AGENAC. . . (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                   S2 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REBEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
S6 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 2326;
Pred. No. 2.8e+02;
5; Mismatches 4; Indels
 CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     D58DEAA09E819B6B CRC64;
                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. Rep. 13:333-335(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL 52.1 KDA PROTEIN YCF80 (ORF450).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 AA.
                                                                                                                                                                     POLY-GLN.
                                                                                                                                                                                  POLY-HIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%;
42.1%;
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839 PESCEAPRRS--HRHRDKL 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                              2046
388
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                                                                                                                                                                              371
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1869
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271
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YC80_PORPU
ID YC80_PORPU
P51218;
'OCT-199'
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TRANSMEM
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CA_BIND
CARBOHYD
             FRANSMEM
                                                               PRANSMEM
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VASP_MOUSE
                                                                                                                                                                                                                                                               STRAIN=129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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                                          Matches
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                         Petunia hybrida (Petunia).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Pepermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae: euasterids I; Solanales; Solanaceae; Petunia.
NCBL_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                    .i. SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ranscription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                      ;
                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FLORAL HOMEOTIC PROTEIN PMADS 1 (GREEN PETAL HOMEOTIC PROTEIN).
                                                   DB 1; Length 450;
        Hypothetical protein; Chloroplast,
SEQUENCE 450 AA; 52127 MW; 800F6FF8D5606C7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 K-BOX.
27039 MW; 76AE5E0B4348BB6F CRC64;
                                                                                                                                                            231 AA.
                                               11arity 53.8%; Score 40.5; Iniarity 53.8%; Pred. No. 60; Conservative 5; Mismatches
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                          LESS IN CARPELS AND SEPALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4endel; 9804; PEThy; MADS; 3.
InterPro; IPR002487; K-box.
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X69946; CAA49567.1; -. PIR; S31693; S31693.
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EMBL; U38804; AAC08104.1;
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fam; PF01486; K-box; 1.
fam; PF00319; SRF-TF; 1
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292 QQAKNL-HFHENQ 303
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TRANSFAC; T01777; -
                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                      8 QOARNVOHYHKNE
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 TISSUE-Petal
                                                                                                                                                           MAD1_PETHY
Q07472;
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MEDLINE-99185054; PubMed-10085070;
MCDLINE-99185054; PubMed-10085070;
MCDLINE S.P., Uhler M.D.;
"Cyclic AMP- and cyclic GMP-dependent protein kinases differ in their regulation of cyclic AMP response element-dependent gene transcription.";
J. Biol. Chem. 274:8391-8404(1999).

-:-FUNCTION: ACTIN- AND PROFILIN-BINDING MICROFILAMENT-ASSOCIATED PROTEIN. MAY ACT IN CONCERT WITH PROFILIN TO CONVEY SIGNAL TRANSDUCTION TO ACTIN FILAMENT PRODUCTION (BY SIGNAL TRANSDUCTION TO ACTIN FILAMENT PRODUCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of the VASP (vasodilator-stimulated phosphoprotein) genes in human and mouse: structure, sequence, and chromosomal localization."; Genomics 36:227-233(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-:- SUBCELLUAR LOCATION: FOCAL ADHESIONS (BY SIMILARITY).
-:- PTHM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT PROTEIN KINASE (CGPK) IN PLATELETS.
                                                                   Gaps
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PHOSPHORYLATION (BY CAPK AND CGPK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY CAPK AND CGPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96411679; PubMed-8812448;
Zimmer M., Fink T., Fischer L., Hauser W., Scherer K., Lichter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO.
POLY-SER.
PHOSPHORYLATION (BY CAPK AND CGPK)
                                                                      ö
Similarity 33.3%; Score 40; DB 1; Length 231; Similarity 33.3%; Pred. No. 35; 7; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    P70460; Q9R214;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A., AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF084548; AAD16045.1; -.
AGD; MGI:109268; Vasp.
InterPro; IPR000697; RanBPL_WASP.
InterPro; IPR001960; WH1.
                                                                                                                                                                                145 NQIETFKKKVRNVEEIHRNLL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Actin-binding
                                                                                                                                      21
                                                                                                                                      1 NSPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X98475; CAA67108.1;
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00568; WH1; 1.
SMART; SM00461; WH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
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PRT;

STANDARD;

379 EQPAEVVEYSKNE 392

7 EQQARNVQHYHKNE 20

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SNX8_HUMAN
Q9Y5X2;
                                                                                                                                          RESULT 25
SNX8_HUMAN
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DITAL PAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. TIG SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIENCE 269:496-512(1995).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. ACTS AS A CHAPERONE BY MAINTAINING THE NEWLY SYNTHESIZED PROTEIN IN AN OPEN CONFORMATION
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95350630; PubMed=7542800; Relative D. Clayton R.A., Kirkness E.F., Reilavage A.R., Bult C.J. Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heddlom E. Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00254; FKBP; 1.
PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
Cell division; Chaperone; Isomeraes; Rotamase; Complete proteome.
                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                    Score 40; DB 1; Length 376;
Pred. No. 59;
                                                                                                                                                                                                      Indels
                              T -> A (IN REF. 2).
MISSING (IN REF. 2).
CC338D07519A0294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 PPIASE, FKBP-TYPE.
48332 MW; C6DB71F502973096 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRIGGER FACTOR (TF).
                                                                                                                                                                                                   3; Mismatches
          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001179; FKBP_PPIase.
                                                                           39824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                 33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32754; AAC22370.1; -.
                                                                                                                                                                                                                                                                                      134 SPEELEOOKROPEHMER 150
                                                                                                                                                                                                                                            2 SPDSCEQQARNVQHYHK 18
                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32,
                                                                           376 AA;
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIG OR HI0713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HI0713:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                               TIG_HAEIN
P44837;
                      CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
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                                                                                                                                                                                            Matches
5113
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                                                                                                                                                                                                                                                            "Identification of eleven novel human sorting nexin molecules, A sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :
0
                                                                                                                                                                                                                                                                                     group of the sorting nexin family is associated with the early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 465;
Pred. No. 74;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52569 MW; 90C5EDB761C31E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
01-NoV-1995 (Rel. 340, Last annotation update)
PUTATIVE HISTONE DEACETYLASE CO8811.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 AA.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Teasdale R.D., Gleeson P.A., Karlsson L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF121858; AAD27831.1; -. InterProx; IRPO01683; PX. Pfam; PF00787; PX; 1. SWART; SM00312; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport; Protein transport.
DOMAIN 72 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 DLCERHEKGVLHKHQRAL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 DSCEQOARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 38.5.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Simms M.;
                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                             TRAFFICKING.
                                                                   SORTING NEXIN 8.
                                                                                                                                                                                                                                                                                                              endosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDA2_CAEEL
Q09440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
HDA2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C08B11
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Gaps

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Indels

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.2; Mismatches

8; Conservative

Query Match Best Local Similarity Matches 8; Consery

33.9%; Score 40; DB 1; Length 432; 57.1%; Pred. No. 68;

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MEDLINE=97344368; PubMed=9200815;
Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C., Schwager C., Paces V., Sander C., Ansorge W.;
"DNA sequencing and analysis of 130 kb from yeast chromosome XV.";
Yeast 13:655-672(1997).
                                                                                                                                                                                                                                                                  HSSP; P08047; 1SP2.
InterPro; IPRO10822; Znf-C2H2.
Pfam; PF00065; Zf-C2H2; 20.
PRINTS; PR00048; ZINCFINGER.
PROSTE; SM00355; Znf-C2H2, 18.
PROSITE; PS01028; ZINC_FINGER_C2H2_1; 17.
PROSITE; PS510157; ZINC_FINGER_C2H2_2; 18.
PROSITE; PS10101 regulation; DNA-binding; Zinc-finger; Metal-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARPB OR YOR141C OR YOR3348C.
Saccharonyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H -> Y (IN REF. 2).
E -> K (IN REF. 2).
DFDFF4741DAEBC7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C2H2 - TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC FINGE
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM.
                                                                                                                                                                                                                               EMBL; AC021092; AAF24968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556
72374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::||::||::
47 COTEARTICNSHKTEI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 CEQQARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-LIKE PROTEIN ARP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344
372
400
400
428
486
512
596
633
856
623
856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARP8_YEAST
ID ARP8_YEAST
AC Q12386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                         FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4). HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Han Z.-G., Zhang Q.-H., Ye M., Kan L.-X., Gu B.-W., He K.-L., Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z.; "Molecular cloning of six novel Kruppel-like zinc finger genes from hematopoletic cells and identification of a novel transregulatory domain KRNB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.HUMAN
2255_HUMAN STANDARD; PRT; 623 AA.
09UID9; 09Y2P6;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ZINC FINGER PROTEIN 255 (BONE MARROW ZINC FINGER 2) (BMZF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 507
Pred. No. 81;
6; Mismatches 7; Indels
                 Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Nuclear protein.
F500D405F7595BAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 274:35741-35748(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; C08B11.2; CE01472.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Bone marrow;
MEDLINE-20054457; PubMed-10585455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 protein; Hydrolase;
507 AA; 57138 MW; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%;
Similarity 31.6%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 : ||| : : ||| :|: :: 21 PDGADVKKRNVAYYYHKDV 39
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                                                                                                                                                                                                                                       FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 246676; CAA86662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZNF255 OR BMZF2
                                                                                                                                                        SIMILARITY)
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SEQUENCE 50
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                                                   Poch O., Winsor B.; "Who's who among the Saccharomyces cerevisiae actin-related proteins? A classification and nomenclature proposal for a large family."; Yeast 13:1053-1058(1997).
-1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-5288C;
MEDLINE-94378723; PubMed-8091862;
Rasmusson S.W.
"Sequence of a 28.6 kb region of yeast chromosome XI includes the FBA1 and TOA2 genes, an open reading frame (ORF) similar to a translationally controlled tumour protein, one ORF containing motifs also found in plant storage proteins and 13 ORFs with weak or no homology to known proteins.";
Yeast 10:563-568(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288C;
MEDLINE=94205268; PubMed=8154189;
MEDLINE=94205268; PubMed=8154189;

"The Sequence of a 17.5 kb DNA fragment on the left arm of yeast chromosome XI identifies the protein kinase gene ELM1, the DNA primase gene PRI2, a new gene encoding a putative histone and seven new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 103.1 KDA PROTEIN IN NUF120-CSE4 INTERGENIC REGION.
YKL050C OR YKL301 OR YKL263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%; Score 40; DB 1; Length 881; 35.3%; Pred. No. 1.4e+02; ative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          881 AA; 100208 MW; 8174851B6B077A19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                   MEDLINE-97435478; PubMed-9290209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: TO YEAST YMR031C.
                                                                                                                                                                                                                                                                                                                                                                                                       Structural protein; Cytoskeleton
                                                                                                                                                                                                                                                                                                         EMBL; X94335; CAA64058.1; -. EMBL; Z75049; CAA99341.1; -. SGD; S0005667; ARP8. InterPro: IPR000279; Actin. SMART; SM00268; ACTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 410-922 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-452 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 EELEEQHQNIEHQNGNE 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.9
Best Local Similarity 35.3
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKFO_YEAST
P35736;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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MEDLINE=94186507; PubMed=8138542;
Watanabe Y., Kawakami K., Hirayama Y., Nagano K.;
"Aranscription factors positively and negatively regulating the Na,K-ATPase alpha 1 subunit gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: EXPRESSED IN HEART AND SKELETAL MUSCLE, BUT
NOT IN LIVER, SPLEEN, OR PANCREAS.
-i- SIMILARITY: BELONGS TO DELTA-EFI/ZFH-1 FAMILY OF TWO-HANDED ZINC
FINGER/HOMEODOMAIN PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BΕ
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"A human zinc finger homeodomain protein homologous to the chicken delta-crystallin enhancer binding protein, delta EFI.";
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression.";
Science 254.1791-1794(1991).
-!- FUNCTION: INHIBITS INTERLEUKIN-2 (IL-2) GENE EXPRESSION. MAY BE RESPONSIBLE FOR TRANSCRIPTIONAL REPRESSION OF THE IL-2 GENE.
BENHANCES OR REPRESSES THE PROMOTER ACTIVITY OF THE ATPLA1 GENE.
DEPENDING ON THE QUANTITY OF CDNA AND ON THE CELL TYPE.
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 390-1124 FROM N.A. MEDILINE-92108424; PubMed=1840704; MEDILINE-92108424; PubMed=1840704; Williams T.M., Moolten D., Burlein J., Romano J., Bhaerman R., Godillot A., Mellon M., Rauscher F.J. III, Kant J.A.; "Identification of a zinc finger protein that inhibits IL-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCF8_HUMAN STANDARD; PRT; 1124 AA. P37275; Q13800; Q12924; D1-0CT-1994 (Rel. 30, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) TRANSCRIPTION FACTOR 8 (NIL-2-A ZINC FINGER PROTEIN) (NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length x2.
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                   EMBL; X71621, -; NOT_ANNOTATED_CDS.
EMBL; Z28050; CAA81885.1; -.
PIR; S37871, S37871.
PIR; S37871, S47871.
Hyporhetical protein.
SEQUENCE 922 AA; 103143 MW; 362EE9A3F642DC8B CRC64;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Bachman N.J., Scarpulla R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%;
37.5%;
                                                                                                                                                                                                                                          EMBL; X75781; CAA53420.1; -.
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547 DACERDLKNSSIEHYY 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.9
Best Local Similarity 37.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATOR OF IL2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M.; The sequence of a 17,933 bp segment of Saccharomyces cerevisiae chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and five
                                                                                                                                                             Pram; PR00096; Zf-CZHZ; 7.

PRINTS; PR00048; ZINCFINGER.

SMART; SM00389; HOX; 1.

PROSITE; PS00028; ZINC_FINGER_CZHZ_1; 5.

PROSITE; PS0157; ZINC_FINGER_CZHZ_1; 5.

PROSITE; PS0157; ZINC_FINGER_CZHZ_2; 6.

HOMEODOX; Repressor; Activator; Metal-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fung1; Ascomycòta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    new open reading frames.";
Yeast 12:485-491(1996).
-!- SUBCELLUAR LOCATION: INTECRAL MEMBRANE PROTEIN (POTENTIAL)
-!- SIMILARITY: CONTAINS 3 C2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
WHYPOTHETICAL 132.5 KDA PROTEIN IN TOP2-MKT1 INTERGENIC REGION.
YNLO87W OR N2250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . S (IN REF. 3).
0A2714CC37C848D1 CRC64;
                                                                                                                                                                                                                                                                                                                    C2H2-TYPE (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                     (IN REF. 2).
(IN REF. 3).
(IN REF. 2).
(IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                      -> I (IN REF. 3
-> Q (IN REF. 3
-> T (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                        GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1178 AA
                                                                                                                                                                                                                                                                                                                                 HOMEOBOX-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                           C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                 C2H2-TYPE.
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                                                                 EMBL, D15050, BAA03646.1; -.
EMBL, U12170, AAA20602.1; -.
EMBL, M81699; -; NOT_ANNOTATED_CDS.
HSSP; P08046; 1A1F.
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STRAIN-S288C / FY1679;
MEDLINE-96310628; PubMed-8740422;
                                                                                                                                     InterPro; IPR001356; Homeobox.
InterPro; IPR000822; Znf-C2H2.
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Best Local Similarity
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P48231;
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DNA_BIND
ZN_FING
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ZN_FING
ZN_FING
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YNI7_YEAST
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Matches
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            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheret G., Sor F.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + PHOSPHATE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY V.
European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cziepluch C., Jauniaux J.-C., Kordes E., Poirey R., Pujol A.
                                                                                                                                                                                                                                                                                                                                                                                              Length 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                     6597DE191C739F41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE CATION-TRANSPORTING ATPASE 2 (EC 3.6.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                               2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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C2 DOMAIN 2.
C2 DOMAIN 3.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                           Transmembrane;
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                                                                                                                                                                          SM00239, C2; 4.
; PS50004; C2_DOMAIN_2;
tical protein; Transmemb
                                                                                   EMBL; X89016; CAA61423.1; -.
EMBL; Z71363; CAA95963.1; -.
HSSP; P21707; IRSY.
SGD; S0005031; YNL087W.
InterPro; IPR000008; C2.
Pfan; PF00168; C2; 4.
SWART; SW00239; C2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                 33.9%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                        AA;
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Q12697;
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TRANSMEM
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Matches
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RESULT 34
YD54_AQUAE
ID YD54_AQUAE
AC 067367;
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                                            Hypothetical protein; Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding
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                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY), MAGNESIUM (BY SIMILARITY), BY SIMILARITY), BY SIMILARITY, BY SIMILARITY, G738AC22E561A449 CRC64;
                                                                                                                                                                                                                                                                                                                                                          33.5%; Score 39.5; DB 1; Length 1472; 40.9%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 17.0 KDA PROTEIN IN COTF-TETB INTERGENIC REGION.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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      InterPro; IPR001454; Hydrolase.
Pfam; PF00122; E1-E2_ATPass; 1.
Pfam; PF00702; Hydrolase; 1.
PROSITE; PS00154; ATPASE_E1_E2; 1.
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InterPro; IPR001757; E1-E2_ATPase.
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1264
1271
1289
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1331
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1472 AA;
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Best Local Similarity
Lace 9; Conserve
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1375
1388
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ID YYAT_BACSU
AC P37504;
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TRANSMEM
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             Usage by
                                                                                                                                                                                                                                  11 protein; Complete proteome.
148 AA; 17003 MW; 72CDB9A50800A9F3 CRC64;
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SEQUENCE 150 AA; 17338 MW; 490C48DB6F952BCF CRC64;
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                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1;
Pred. No. 32;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE UPF0054 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
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InterPro; IPR000182; Acetyltransf_GCNS.
Ham; PF00583; Acetyltransf; i.
Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=98196666; PubMed=9537320;
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                                                                                                                                                                                                                                                                                                                                       33.18; 29.48;
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PROSITE; PS01306; UPF0054; 1.
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                                                                                               EMBL; D26185; BAA05203.1;
EMBL; Z99124; CAB16109.1;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.4*
Matches 5; Conservative
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39 DTLQEQCQHILVYHENQ 55
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Matches 8; Conservative
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Biochem. J. 278:203-209(1991)
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P48569;
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SEQUENCE
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YDB3_YEAST
   SOUTH THE THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT THE TENT TO THE TENT THE T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91354204; PubMed-1883330; Cannons A.C., Idda N., Solomonson L.P.; "Expression of a cDNA clone encoding the haem-binding domain of Chlorella nitrate reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                           Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN VESICULAR PROTEIN TRAFFICKING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 225; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
04F746798C48EAC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01105; EMP24_GP25L; 1. Transmembrane; Signal; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETICULUM (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERP3 PROTEIN.
LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NITRATE REDUCTASE (EC 1.6.6.1) (NR) (FRAGMENY).
                                                                                                                 15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ERP3 PROTEIN PRECURSOR.
ERP3 OR YDL018C OR D2850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AA.
                              225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000348; Emp24_gp25L_p24.
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                              PRT;
                                                                                         (Rel. 37, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 248432; CAA88341.1; -. EMBL; 274066; CAA98576.1; -. SGD; S0002176; ERP3.
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26511 1
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                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlorella vulgaris
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C;
                                                                                      15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIA_CHLVU
Q01170;
                           ERP3_YEAST
Q12403;
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   ERP3_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEETE WAS DRANGED COUNTY OF THE STEETE STANK AND DESCRIPTION OF THE STANK AND DESCRIPTION OF THE
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-!- FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED IN THE FIRST
                                                                                                                                                                                                                                                                                                -1- SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
-1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                               STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.
-!- CATALYTIC ACTIVITY: NADH + NITRATE = NAD(+) + NITRITE + H(2)O.
-!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FPHEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
                                                                                                                                                                                                                                  -i-SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN IN RPL41A-INH1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS00559; CYTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum; NON The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEME LIGAND (BY SIMILARITY). HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34830 MW; E60D82FE1E98292A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1;
Pred. No. 71;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001199; Cyt_B5.
InterPro; IPR000572; Euk_oxidored_molyb.
Pfam; PF00173; heme_1; 1.
Pfam; PF00174; oxidored_molyb; 1.
                                                                                                                                                                          GROUP IS CALLED CYTOCHROME B-557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-96021607; PubMed-8533471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
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31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X56771; CAA40090.1; -. PIR; S17197; S17197. HSSP; P04166; 1B5M.
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Best Local Similarity 31.6
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                             -!- SUBUNIT: HOMODIMER
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last sequence update)
40-MG-2001 (Rel. 40, Last annotation update)
GRB2-RELATED ADAPTOR PROTEIN 2 (GADS PROTEIN) (GRB4H FACTOR RECEPTOR
BINDING PROTEIN) (GRB4G) (GRB2-LIKE PROTEIN) (GRB2L) (HEMATOPOIETIC
CELL-ASSOCIATED ADAPTOR PROTEIN GRPL) (GRB-2-RELATED MONOCYTIC ADAPTER
PROTEIN) (MONOCYTIC ADAPTER) (MONA) (ADAPTER PROTEIN GRID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kedra D., Dumanski J.P.;
"Cloning of the human and mouse growth factor receptor binding protein
like genes.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'GRID, a novel Grb2-related adapter protein which interacts with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu S.K., McGlade C.J.;
"Gads is a novel SH2 and SH3 domain-containing adaptor protein that binds to tyrosine-phosphorylated Shc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mona, a novel hematopoietic-specific adaptor interacting with the macrophage-colony-stimulating factor receptor, is implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellis J.H., Ashman C., Burden M., Kilpatrick K.E., Morse M.A.,
Hamblin P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Law C.-L., Ewings M.K., Chaudhary P.M., Solow S.A., Yun T.J.,
Marshall A.J., Hood L., Clark E.A.;
"GrpL, a Grb2-related adaptor protein, interacts with SLP-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1; Length 320;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bourette R.P., Arnaud S., Myles G.M., Rohrschneider L.R.,
Blanchet J.P., Mouchiroud G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocyte/macrophage development.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              EMBL; X83276; CAA58263.1; -.
EMBL; Z74231; CAA98758.1; -.
SGD; S0002342; YDL183C.
Hypothetical protein.
SEQUENCE 320 AA; 37047 MW; C287FD3350D3D301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulate NF-AT activation.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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Oncogene 17:3073-3082(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-99087328; PubMed-9872323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||| | :| : : ||||
169 SSPDECLROMKKLYQEGLIYHK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NSPDSCEQQARNVQH----YHK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRP2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
   TE STATE STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
activated T cell co-stimulatory receptor CD28.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH SLP-76 TO REGULATE NF-AT ACTIVATION.
BINDS TO TYROSINE-PHOSPHORYLATED SHC.
-!- SIMILARITY: CONTAINS 1 SLD DOMAINS.
-!- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zhu Y.,
Kelsell D.P., Murdock P.R., Herrity N.C., Lewis C.J., Cross D.A.,
Culbert A.A., Reith A.D., Barnes M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 322;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H3 2.
736311D0640CD3D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WNT4_HUMAN STANDARD; PRT; 351 AA. P56705; Q9GUM2; Q9H1J8; [15-JUL-1999 (Rel. 38, Created) 20-MG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF055465; AA008803.1; --
EMBL; AF053405; AAC98669.1; --
EMBL; AF129477; AAD41783.1; --
EMBL; AF236118; AAF60318.1; --
HSSP; P29544; IGRI.
MGD; MGI:1333842; Mona.
InterPro; IPR000980; SH2.
InterPro; IPR0001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ011735; CAA09756.1; -.
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36810 MW;
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50.0%;
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Pfam; PF0018; SH3; 2.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50001; SH2; 1.
SH2 domain; SH3 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.1
Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1| | :||:|
214 QQQRYLQHFHQD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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SEQUENCE
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      A THE TENT OF THE 
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FUNCTION: MAY BE AN INTRACELLULAR SIGNALING MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY). SEEMS TO BE INVOLVED IN KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE-91122634; PubMed-2279700;
Gavin B.J., McWahon J.A., McMahon A.P.;
"Expression of multiple novel Wnt-1/int-1-related genes during fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                              Huguet E.L., McMahon J.A., McMahon A.P., Bicknell R., Harris A.L., "Differential expression of human Wnt genes 2, 3, 4, and 7B in human breast cell lines and normal and disease states of human breast
                                                                                                                                                              Cancer Res. 54:2615-2621(1994).

Cancer Res. 54:2615-2621(1994).

-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY). OVEREXPRESSION MAY BE ASSOCIATED WITH ABNORMAL PROLIFERATION IN HUMAN BREAST TISSUE.

-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%; Score 39; DB 1; Length 351; 63.6%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> T (IN REF. 2).
-> F (IN REF. 2).
25072318EDF1F93A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
WNT-4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                              MEDLINE-94221588; PubMed-8168088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and adult mouse development.";
Genes Dev. 4:2319-2332(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY009398; AAG38658.1; -. EMBL; AL031281; CAB52601.1; -. MIM; 603490; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39029 MW;
             [3]
SEQUENCE OF 210-329 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000970; Wntl.
Pfam; PF00110; wnt; 1.
PRINTS; PR01349; WNTPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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297 . 29
106 10
111 13
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P22724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lacher M.D., Walther P.R., Lareu R., Dharmarajan A.M., Friis R.R.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE AN INTRACELLULAR SIGNALING MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO SIGNAL OVER ONLY FEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL DIAMETERS (BY SIMILARITY).
SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
DEVELOPMENT.

-!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.

-!- TISSUE SPECIFICITY: IN ADULTS IN LUNG AND BRAIN.

-!- SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WNT-4 PROTEIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
7EICŚC739BE939D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1;
Pred. No. 79;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-4NG-2001 (Rel. 40, Created)
20-4NG-2001 (Rel. 40, Last sequence update)
20-4NG-2001 (Rel. 40, Last annotation update)
WNT-4 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI 98957; Wnt4.
InterPro: IPR000970; Wnt1.
Pfam; PF00110; Wnt; 1.
SMART; SM00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
SNGALD: PS00246; WNT1; 1.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Corpus luteum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M89797; AAA40566.1; -.
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Best Local Similarity 63...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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351
88
297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SPDSCEQQARN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNT4_RAT
Q9QXQ5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hume C.R., Dodd J.;
"Cwnt-8C: a novel Wnt gene with a potential role in primitive streak formation and hindranal organization.",
Development 119:1147-1160(1993).

-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS. MAY BE INVOLVED IN THE REGULATION OF AXIS FORMATION AND IN THE RHOMBOMERE SPECIFICATION.

-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: CELLS THAT FORM RHOWBOWERE 4. HENSEN'S NODE AND THE NEURAL PLATE IMMEDIATELY ANTERIOR TO IT.
-i- DEVELOPMENTAL STRAGE: EXPRESSED DURING EMBRYOGENESIS.
-i- SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
5F8D80C3B4502BA1 CRC64;
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WNT-8C PROTEIN.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                             1; Length 351;
                                                                                                                                                                                                                                                                              3; Indels
        EMBL; AF188608; AAF15589.1; -.
InterPro; IPR000970; Wnt1.
Pfam; PF00110; wnt; 1.
SWART; SW00097; WNT1; 1.
PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein; Signal.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 351 WNT-4 PROTEIN.
CARBOHYD 297 297 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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SIGNAL 16 POTENTIAL.
CHAIN 17 357 WNT-8C PROTEIN.
CARBOHYD 104 N-LINKED (GLCNAK
CARBOHYD 263 263 N-LINKED (GLCNAK
                                                                                                                                                                                                                                         Score 39; DB 1
Pred. No. 79;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNT-8C PROTEIN PRECURSOR (CWNT-8).
WNT-8C.
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MEDLINE-94139558; PubMed-7916678;
                                                                                                                                  23 351 WW
88 88 N-
297 297 N-
351 AA; 39043 MW;
                                                                                                                                                                                                                                         33.1%;
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Pfam; PF00110; wnt; 1.
SWART; SM00097; WNTl; 1.
PROSITE; PS00246; WNTl; 1.
                                                                                                                                                                                                                                    Query Match 33.1
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
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276 SPDFCEQDMRS 286
                                                                                                                                                                                                                                                                                                         2 SPDSCEQQARN 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
WN8C_CHICK
P51030;
                                                                                                                                                                                    SEQUENCE
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Yokoi H., Nishimatsu A., Ozato K., Yoda K.;
Submitted (AnG-1997) to the EMBL/Genbark/DBU databases.

-!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN MAY BE A SIGNALING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryzias latipes (Medaka fish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
Beloniformes, Adrianichthyldae, Oryzinae, Oryzias.
      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
58ADD7E835A5B8C4 CRC64;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
E9864E1FA342E82D CRC64;
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                                                                                                                                                      Score 39; DB 1; Length 357
Pred. No. 80;
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MN5B_ORYLA

ID WN5B_ORYLA

AC 042122

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental protein; Glycoprotein; Signal. SIGNAL 1 28 POTENTIAL.
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                                                             40042 MW;
                                                                                                                                                                                                                                                                     21
                                                                                                                                                      33.1%;
42.9%;
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                                                                                                                 Ouery Match
Best Local Similarity 42.3%
Best Local 9, Conservative
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282
346
357 AA;
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Best Local Similarity
Matches 7; Conserv
CARBOHYD
CARBOHYD
SEQUENCE
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LDLR_CRIGR

LD LDLR_CRIGR

AC P35950;
DT JUN-1994 (Rel. 29, Created)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DF 20-AUG-2001 (Rel. 40, Last annotation update)
DF 20-AUG-2001 (Rel. 40, Last annotation update)
DF LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
GN LDLA.
OS Cricerulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                        Bishop R.W.;
"Structure of the hamster low density lipoprotein receptor gene.";
J. Lipid Res. 33:549-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. .
LOW-DENSITY LIPOPROTEIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein, LDL, Cholesterol metabolism; Lipid transport;
Endocytosis; Coated pits; Transmembrane; Receptor; Signal;
EGF-like domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M94387; 'AAA51449.1, -.
EMBL, M1877; -; NOT_ANNOTATED_CDS.
PIR; A48908; ORHVID.
HSSP, P01130; ILDR.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR00151; EGF-11ke.
InterPro; IPR00151; EGF-11ke.
InterPro; IPR00137; LDL_recept_A.
InterPro; IPR00172; LDL_recept_A.
Ffam; PF00067; Idl_recept_a; 7.
Pfam; PF00057; Idl_recept_a; 7.
Pfam; PF00057; Idl_recept_a; 7.
Pfam; PF00057; Idl_recept_b; 5.
PRNWTS; SM00179; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00192; LDLR: 2.
SMART; SM00192; LDLa: 7.
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                                                                                                                                                                                                                         NCBI_TaxID-10029;
                                                                                                                                                                                                         Cricetulus.
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LDL-RECEPTOR CLASS B 1.

LDL-RECEPTOR CLASS B 2.

LDL-RECEPTOR CLASS B 3.

LDL-RECEPTOR CLASS B 4.

LDL-RECEPTOR CLASS B 5.

LDL-RECEPTOR CLASS B 5.

LDL-RECEPTOR CLASS B 6.

LDL-RECEPTOR CLASS B 7.

LDL-RECEPTOR CLASS B 6.

LDL-RECEPTOR CLASS B 7.

LDL-
                                                                       LDL-RECEPTOR
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Pred. No. 2e+02;
5; Mismatches 6; Indels
                                              CYTOPLASMIC (POTENTIAL).
7 X 41 AA TANDEM REPEATS OF 1
CLASS DOMAIN; LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5D50EBFDD834B35E CRC64;
EXTRACELLULAR (POTENTIAL)
                                                                                                               LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AA.
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EGF-LIKE 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 45
PH87_YEAST
ID PH87_YEAST STANDARD; I
52 P25360;
DT 01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.1%;
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 PDTCDQLCVNLEGSYKCE 379
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                                                                                                                    244.
2256.
2277.
2297.
3319.
3359.
3359.
3657.
697.
677.
657.
854. AA;
  22
783
805
25
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between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                          01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 105.9 KDA PROTEIN IN RPLISB-GCR3 INTERGENIC REGION.
TWR124W OR YM8564.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AGG-2001 (Rel. 40, Created)
20-AGG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 943.
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                 Lye G., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                    Pandit S., Sternglanz R.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER. ; 6631BEFBCD62E601 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         943 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1405 AA
                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN.
POLY-GLY.
POLY-GLY.
POLY-ASP.
POLY-GLN.
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 770-943 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z49273; CAA89273.1; -. EMBL; L07650; AAA35122.1; -. PIR; S48514; S48514. SGD; S0004731; YMRL24W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.1%;
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          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
536
715
943 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces
NCBI_TaxID=4896;
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                                                                                                                                                                               NCBI_TaxID=4932;
        YM11_YEAST
P39523;
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094666;
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RPC1_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                             r. Genet. 29:344-351 (1996).
FUNCTION: INVOLVED IN THE UPTAKE OF INORGANIC PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENITAL).
SIMILARITY: BELONGS TO THE NADC/P/PHO87 FAMILY OF TRANSPORTERS.
PHO87 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                             new genes, PHO86 and PHO87, involved in inorganic phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL).
                                                                                                                                                                                                     Thierry A., Fairhead C., Dujon B.; "The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORFs, including a gene for a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.1%; Score 39; DB 1; Length 923; llarity 42.9%; Pred. No. 2.2e+02; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D168FC52FE26C5CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
01-MAY-1992 (Rel. 22, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
1008GANIC PHOSPHATE TRANSPORTER PHOB7.
PHOB7 OR YCR037C OR YCR374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                 uptake in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                            MEDLINE-96171517; PubMed-8598055;
                                                                                                                                                                                      MEDLINE-91181345; PubMed-1964349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X56909; CAA40229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102549
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                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DSCEQQARNVQHYH 17
                                                                                                                                                                                                                                                                            (east 6:521-534(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphate transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S12919; MMBY7C
S0000633; PHO8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                     NCBI_TaxID-4932;
                                                                                                                                                                                                                                                            ribokinase."
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TRANSMEM
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TRANSMEM
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PIR; SGD;

JWO

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Gaps

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Length 943;

Wood V., Rajandream M.A., Barrell B.G., Volckaert G., Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

RESULT 46 YM11_YEAST

24

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE III (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

MISCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

MISCELLULAR BUKARYOTIC NUCLEI: POLYMERASE IFOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR SAND TRNA GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93281390; PubMed-8506138; Yangaz R.J., Vinuela E.; Yangaz R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.; African swine fever virus encodes two genes which share significant homology with the two largest subunits of DNA-dependent RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.; "Analysis of the complete nucleotide sequence of African swine fever
                         CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                             InterPro: IPR000722; RNA_pol_A.
InterPro: IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A7; 1.
Pfam; PF01854; RNA_pol_A2; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Length 1405;
Pred. No. 3.4e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         1405 AA; 157561 MW; 104B1AC4145A3B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Asfarviridae; African swine fever-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT 1 (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                               C3H-TYPE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 21:2423-2427(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-DEC-1998 (Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                   EMBL; AL035570; CAB37604.1; -
                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 208:249-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            1385
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| 808 QDRSLPHFHKN 818
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                                                                                                                                                                                                                                                                                                                                                                                                            1381
            SUBSTRATES
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P42486;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
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                                                       -!- SIMILARITY: TO THE CORRESPONDING SUBUNITS OF PROKARYOTIC AND EUKARYOTIC RNA POLYMERASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAC_SCHPO STANDARD; PRT; 2280 AA.
P78820; Q09447; Q09576; Q09667; Q09616; O94557;
15-JUL-1998 (Rel. 36, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
ACGTYL-COA CARBOXYLASE (EC 6.4.1.2) (ACC) [INCLUDES: BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .Length 1450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA directed RNA polymerase, Transcription.
450 AA; 163748 MW; 94D335C50B9A281B CRC64;
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to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Ler
Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1450 AA; 163748 MW;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000722; RNA_pol_A.
InterPro; IPR000879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A1.
Pfam; PF01854; RNA_pol_A2; 1.
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illarity 57.1%;
Conservative
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CUT6 OR SPAC56E4.04C.
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Submitted (DEC-1996)
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Matches 8; Conserv
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SEQUENCE FROM N.A.
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SUBSTRATES
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COAC_SCHPO
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-!- COFACTOR: BIOTIN

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SEQUENCE OF 1-14 FROM N.A.
STRAIN=168 / JH642;
MEDLINE-92235865; PubMed=1569582;
GONZY-Treboul G., Karmazyn-Campelli C., Stragier P.;
"Developmental regulation of transcription of the Bacillus subtilis ftsAz operon.";
J. Mol. Biol. 224:967-979(1992).
                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
MEDLINE-89008108; PubMed=3139638;
Beall B., Lowe M., Lurkenhaus J.;
"Cloning and characterization of Bacillus subtilis homologs of Escherichia coli cell division genes ftsZ and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
                                                             FTSA_BACSU STANDARD; PRT; 440 AA. P28264; Q45573; 01-DEC-1992 (Rel. 24, Created) 20-BC-1992 (Rel. 24, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CELL DIVISION PROTEIN FTSA.
                                                                                                                                                                                                      Bacillus subtilis
                         RESULT 50
FTSA_BACSU
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration the European Bioinformatics of Bioinformatics and the EMBL outstationuse by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  ENZME REGULATION: BY PHOSPHORYLATION (BY SIMILARITY).
PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
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InterPro; IRR000081; CpSase.
InterPro; IRR000081; CpSase.
InterPro; IRR000801; CpSase.
InterPro; IRR001602; Carboxyl_trans.
InterPro; IRR00362; Sub_trnsportr.
Pfam; PF00184; blotin_lipoyl; 1.
Pfam; PF00289; Carboxyl_trans; 1.
PROSITE; PS00866; CpSase_L-chain; 1.
PROSITE; PS00867; CpSaSE_1; 1.
PROSITE; PS00867; CpSaSE_2; 1.
PROSITE; PS00867; SpSaSE_2; 1.
PROSITE; PS00867; SpSaSE_2; 1.
PROSITE; PS00867; PSASE_2; 1.
PROSITE; PS00867; PSASE_2; 1.
PROSITE; PS00867; PSASE_2; 1.
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BIOTIN (BY SIMILARITY).
LYARATISLEREPREERTRERMAPRYASHF -> RF
LISOLSISSFSFFILYFINH (IN REF. 3).
F -> S (IN REF. 1).
IEE -> LE (IN REF. 1).
A -> S (IN REF. 1).
A -> T (IN REF. 1).
DNTR -> YRIP (IN REF. 3).
LMKSEPST -> SNEVRIN (IN REF. 3).
                                                      -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: PARTIAL TO CARBAMOYL PHOSPHATE SYNTHETASES.
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EMBL, 299261; CAB16395.1;
EMBL, D83413; BAA11914.1;
EMBL; D83414; BAA11915.1;
EMBL, D83416; BAA11917.1;
EMBL, D83415; BAA11917.1;
HSSP; P24182; IBNC
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InterPro; IPR000089; Biotin
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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SEQUENCE OF 1-8 FROM N.A.

MEDLINE=92325056; PubMed=1624452;
Gholamhoseinian A., Shen Z., Wu J.J., Piggot P.;

Regulation of transcription of the cell division gene ftsA during sporulation of Bacillus subtilis.";

J. Bacteriol. 174-4647-4656(1992).

-i- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT GROWTH (BY SIMILARITY). MAY BE A COMPONENT OF THE SEPTUM. IT MAY INTERACT WITH FTSZ (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE FTSA/WREB FAMILY.
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Pred. No. 1.2e+02;
4; Mismatches 2; Indels
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6064D55961358C44 CRC64;
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Cell division; Cell shape; Complete proteome.
CONFLICT 12 12 L -> I (IN REF.;
SEQUENCE 440 AA; 48102 MW. FORANGEGETTECT.
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EMBL; X66239; CAA46968.1; --
EMBL; S39431, AAD13818.1; --
EMBL; 299111; CAB13401.1; --
Subtilist; BG10231; ftsA.
InterPro; IPR003494; FtsA.
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Best Local Similarity 47.1
Matches 8; Conservative
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Search completed: December 17, 2001, 07:51:58 Job time: 115 sec.

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33.1%; Score 39; DB 1; Length 2280; 43.8%; Pred. No. 5.6e+02; tive 5; Mismatches 4; Indels

Conservative SCEQQARNVQHYHKNE 20

Query Match
Best Local Similarity
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42 35.6 295 2 S58850 42 35.6 408 2 T34467 42 35.6 408 2 T34467 42 35.6 442 2 B81418 42 35.6 498 2 T25934 42 35.6 816 2 D84601 42 35.6 816 2 T46651 42 35.6 1373 2 TEMORE	42 35.6 3191 2 41.5 35.2 321 2 41.5 35.2 337 2 41.5 35.2 463 2 41.5 35.2 692 2 41.4 34.7 188 2 41 34.7 186 2	41 34.7 205 2 41 34.7 229 1 41 34.7 512 2 41 34.7 575 2 41 34.7 589 2 41 34.7 589 2	41 34.7 786 2 41 34.7 792 2 41 34.7 792 2 41 34.7 1103 2	41 34.7 2336 2 40.5 34.3 430 2 40.5 33.9 133 2 40 33.9 147 2 40 33.9 147 2	40 33.9 147 2 40 33.9 231 2 40 33.9 319 2 40 33.9 379 2 40 33.9 389 2	40 33.9 398 2 422 2 422 2 2	40 33.9 432 2 C64088 40 33.9 507 2 T19067	40 33.9 531 2 40 33.9 696 2 40 33.9 796 2 40 33.9 814 2 40 33.9 860 2	40 33.9 881 2 40 33.9 922 2 40 33.9 972 2 40 33.9 1069 2	40 33.9 1124 2 40 33.9 1154 2 40 33.9 1178 2 40 33.9 2437 2	40 33.9 2510 2 40 33.9 4845 2 39.5 33.5 262 2 39 5 33 5 983 2	39.5 33.5 1006 2 39.5 39.5 33.5 2028 2 39.5 33.5 2028 2 39.5 33.5 2051 2 30.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5	39 33.1 148 1 39 33.1 150 2 39 33.1 174 2	39 33.1 181 2 39 33.1 225 2 39 33.1 228 2
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 32 33 OM protein - protein search, using sw model Run on: December 17, 2001, 07:49:38; Search time 12.81 Seconds (without alignments) 38 (without alignments) 38	24.070 Million cell updates/sec	Searched: 219241 seqs, 76174552 residues Total number of hits satisfying chosen parameters: 219241 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	um Match 0% um Match 100% ig first 150 summaries	Database: PIR_68:* 58 1: pir1:* 59 2: pir2:* 60 3: pir3:* 61 4: pir4:* 62	Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Score Match Length DB ID Description	5 41.1 523 2 T19684 hypothetical prote 5 39.0 222 2 S23731 MADS box protein T 38.1 139 2 T09878 albumin 2S storage conserved hypothet transcription fact transcription fact 5 38.1 479 1 S41015 transcription fact hypothetical protein fact transcription fact transcription fact transcription fact fact fact fact fact fact fact fact	44 37.3 185 2 JC7369 prenylated Rab acc 8 44 37.3 227 2 S12378 MADS box protein d 9 44 37.3 358 2 T26281 hypothetical prote	1 44 37.3 640 2 S52047 decxyribodipyrimid 2 44 37.3 734 2 T27055 hypothetical prote 3 44 37.3 778 2 H96649 protein F2401.4 [1 4 44 37.3 800 2 T01843 characteristics	44 37.3 945 2 577052 Cation-transportin 6 43 36.4 139 2 T09850 albumin 2S storage 7 43 36.4 170 2 T02707 probable kinetecho	43 36.4 347 2 730072 hypothetical prote 43 36.4 36.0 2 834173 wht-5c protein - A 440 2 B71858 adenylosuccinate 1 43 36.4 440 2 H64658 adenylosuccinate 1	43 36.4 452 2 745448 probable serine pr 43 36.4 943 2 A42681 centromere protein 42.5 36.0 1002 2 C86026 probable oxidoredu 42.5 36.0 1166 1 E65151 hypothetical 126K 42 35.6 253 2 A65174 hypothetical 28 N	42 35.6 288 2 G75574 TDP-glucose-4,6-de

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albumin 2S storage protein precursor Mat5-A - upland cotton
albumin 2S storage protein precursor Mat5-A - upland cotton
(.Species: Gossypium hirsutum (upland cotton)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 29-Oct-1999
C.Accession: T09878
R.Galau, G.A.; Wang, H.Y.C.; Hughes, D.W.
submitted to the EMBL Data Library, January 1992
A.Description: Cotton Mat5-A (C164) gene and Mat5-D cDNAs encoding methionine-rich 2S
A.Reference number: 216893
A.Reference number: Lanslated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-139 <GAL>
A.Residues: 1-139 <GAL>
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NyAlternate names: floral homeotic protein TM6
C;Species: Lycopersion esculentum (tomato)
C;Species: Lycopersion esculentum (tomato)
C;Date: 27-May-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1999
C;Accession: S23731; S38778
R;Puell, L;Abu-Abeadd, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E. Plant J. 1, 255-266, 1991
A;Title: The MADS box gene family in tomato: temporal expression during floral develo A;Reference number: S23728; MUID:93251098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
C; Superfamily: transcription factor squa; serum response factor DNA-binding domain ho
C; Keywords: DNA binding; nucleus; transcription regulation
F;1-54/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-139/Product: albumin 2S storage protein Mat5-A #status predicted <MAT>
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           Length 523;
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                                                     Indels
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C;Genetics:
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R, Pnueli, L.
Submitted to the EMBL Data Library, July 1991
A, Reference number: S38778
A, Accession: S38778
A, Molecule type: mRNA
A; Residues: 1-159, T7, 161-222 < PNF>
A, Cross-references: EMBL:X60759; NID:g19385; PID:g19386
                                                     9
           Score 48.5; DB 2;
Pred. No. 9.1;
                                                       4; Mismatches
                                                                                                                        3 PDSCEQQARNVQHY-----HKNEL 21
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142 NQTDTCKKKARNLEEQNGN 160
           41.1%;
illarity 32.1%;
Conservative
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Best Local Similarity 36.83
Matches 7; Conservative
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Best Local Similarity 45.8
Matches 11; Conservative
               Ouery Match
Best Local Similarity
Matches 9; Conserv
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A, Molecule type: mRNA
A, Residues: 1-222 <PNU>
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hypothetical protein SCJ1.33 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36966
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M
s;ubmitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Comment: This acceptor, a Rab-interacting Golgi integral membrane protein, function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL109962; PIDN:CAB53151.1; GSPDB:GN00070; SCOEDB:SCJ1.33
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ1.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prenylated Rab acceptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C;Accession: JC7569
R;Liang, Z.; Li, G
Biochem. Biophys. Res. Commun. 275, 509-516, 2000
A;Title: Mouse prenylated Rab acceptor is a novel Golgi membrane protein.
A;Reference number: JC7369
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C;Keywords: brain; Golgi apparatus; membrane protein
                                                                                                                                   DB 1;
29;
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                                                                                                                                   Score 45; DB :
Pred. No. 29;
2; Mismatches
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Pred, No. 15;
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Pred. No.
C; Keywords: DNA binding F;153-340/Domain: T-box homology <TBX>
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36.8%;
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50.0%;
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ilarity 70.0%;
Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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A; Accession: T36966
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Best Local Similarity
Matches 7; Conserva
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| 155 NLFHYHKNEM 164
                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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A: Residues: 1-604 <SEE>
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A; Residues: 1-185 <LIA>
                                                                                                                                                                                                                                                                           12 NVQHYHKNEL 21
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T36966
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R. Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Broon, S.; Broutllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carerer, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Muloo, M.F. Koetter, P.; Kondingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pobl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, S. Schicoter, R.; Scoffone, F.; Sekjauchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wammench, H.; Yamane, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yata, K.; Yasunoto, K.; Yata, K.; Yata, K.; Yasunoto, C.; Roche, B.; Rose, M.; Danchin, A.; Tosato, V.; Ochikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, C.; Roche, B.; Noceston, C.; Roche, C.; Roche, C.; Yoshikawa, H.; Danchin, A.; Mathors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Mathors, C.; Roche, C.; Roche, C.; Roche, C.; Roche, C.; Yoshikawa, H.; Danchin, A.; Mathors, C.; Roche, C.; Mathors, C.; Roche, C.; Yoshikawa, H.; Danchin, A.; Mathors, C.; Roche, C.; Yoshikawa, H.; Danchin, A.; Mathors, C.; Roche, C.; Yoshikawa, M.; Mathors, C.; Mathors
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A; Residues: 1-479 < ABER.
A; Residues: 1-479 < ABER.
A; Cross-references: EMBL: 229443
R; Agulnik, S.I.; Bollag, R.J.; Silver, L.M.
R; Agulnik, S.I.; Bollag, R.J.; Silver, L.M.
A; Title: Conservation of the T-box gene family from Mus musculus to Caenorhabditis elega
A; Reference number: A56530; MUID: 95293375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13575.1; PID:e1185293; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: nucleic acid sequence not shown; not compared with conceptual translation Molecule type: DNA Residues: 153-140 <a href="https://documents.org/lines/not/20140/460">https://documents.org/lines/not/20140/460</a> (Cross-references: GB: Z29443
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Superfamily: Caenorhabditis elegans transcription factor tbx8; T-box homology
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N;Alternate names: hypothetical protein T07C4.2
C;Species: caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S41015; A56530
                                                                                                                                                                                                                                                                                                C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                conserved hypothetical protein ymcA - Bacillus subtilis
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Pred. No. 8.2;
6; Mismatches
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                                                                          34 DSCEQQIRKQAHLKHCQKYMEEEL 57
                            4 DSCEQQARNVQH-----YHKNEL 21
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-143 <KUN>
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7; Indels

Length 604;

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Length 185; Indels

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deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - fruit fly (Drosophila melanogaster) N.Alternate names: DNA photolyase; photoreactivating enzyme C.Species: Drosophila melanogaster C.Species: 5-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S52047
R; Yasuni, A.; Eker, A.P.M.; Yasunira, S.; Yajima, H.; Kobayashi, T.; Takao, M.; Oikawa B; Yasuni, A.; Eker, A.P.M.; Yasunira, S.; Yajima, H.; Kobayashi, T.; Takao, M.; Oikawa EMBO J. 13, 6143-6151, 1994
A; Title: A new class of DNA photolyases present in various organisms including aplace A; Reference number: S52046; MUID:95112825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
NyAlternate names: gp20 protein - phage P22 NyAlternate names: gp20 protein C;Species: phage P22 C;Species: phage R; phage 
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMED:L07556; NID:g215274; PIDN:AAA62407.1; PID:g215276 R;Conlin, C.A.; Vinn, E.R.; Miller, C.G.
J. Bacteriol. 174, 5869-5880, 1992
A;Title: Oligopeptidase A is required for normal phage P22 development. A;Reference number: A43330; MUID:32394890
A;Contents: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:W93985; NID:g215283; PIDN:AAA72116.1; PID:g215286
A;Note: Sequence extracted from NCBI backbone (NCBIN:113001, NCBIP:113005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 56;
6; Mismatches
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C;Superfamily: deoxyribodipyrimidine photo-lyase
C;Keywords: carbon-carbon lyase
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41;
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A;Molecule type: mRNA
A;Residues: 1-640 <7AS>
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Best Local Similarity 36.8
Matches 7; Conservative
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-471 <ADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary A; Molecule type: DNA A; Residues: 1-92 <CON>
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A,Reference number: S19232; MUID:92155166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:X52023; NID:g16019; PIDN:CAA36268.1; PID:g16020
R:Schwarz-Sommer, 2.; Hue, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Tetens, F.; Loennig,
EMBO J. 11, 251-263, 1992
                  MADS box protein defa-1 - garden snapdragon
M.Alternate names: gene deficiens protein
C;Species: Antirrhinum majus (garden snapdragon)
C;Species: Antirrhinum majus (garden snapdragon)
C;Species: 11 Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C;Accession: S12378; S19232
R;Sommer, H.; Beltran, J.P.; Huijser, P.; Pape, H.; Loennig, W.E.; Saedler, H.; Schwarz-Brhud J. 9, 605-613, 1990
A;Title: Deficiens, a homeotic gene involved in the control of flower morphogenesis in P.A;Reference number: S12378; MUID:90183955
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T26281
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Pred. No. 31;
1; Mismatches
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.3°
Best Local Similarity 36.8°
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-358 <WIL>
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A;Introns: 57/3; 320/2
C;Superfamily: unassign
                                                                                                                                                                                                                                                                                                                                                                      Accession: S12378;
Status: preliminary;
Molecule type: mRNA;
Residues: 1-227 <SOM>
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A; Residues: 1-227 <SCH>
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O., K.; Okunura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas Namada, B.; 109-136, 1996
A;Fittle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
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submitted to the EMBL Data Library, January 1992
A;Description: Cotton Mat5 (C164) gene and cDNAs encoding a methionine-rich 2S albumi
A;Reference number: 216886
A;Accession: T09850
                                                                                                                                          A;Map position: 4
A;Introns: 86/1; 173/1; 188/3; 221/3; 246/3; 276/2; 323/2; 347/1; 373/3; 423/3; 443/3
A;Note: F9D12.10
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A; Accession: S77052
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-945 < KARN:
A; Cross-references: EMBL:054005; GB:AB001339; NID:g1001779; PIDN:BAA10744.1; PID:g100
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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*Keywords: hydrolase; ion transport.
:571-741/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cation-transporting ArPase (EC 3.6.1.-) pacL-1 - Synechocystis sp. (strain PCC 6803) N.Alternate names: protein s110672 C; Species: Synechocystis sp. (C; Species: Synariety: PCC 6803 A; Variety: PCC 6803 C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                               Length 800
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  A;Molecule type: DNA
A;Residues: 1-800 <MUR>
A;Cross-references: EMBL:AF077407; NID:g3319339; PID:g3319358
A;Cross-reference: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                            4; Indels
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F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
85;
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                                                                                                                                                                                                                                                                               Score 44; DB 2
Pred. No. 71;
4; Mismatches
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58.8%; Pred. No. 8
                                                                                                                                                                                                                                                                                     37.38;
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.7-
7; Conservative
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667 HSPLPCDPSARNIRH 681
                                                                                                                                                                                                                                                                                                                                                                                                1 NSPDSCEQQARNVQH 15
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Matches 10; Conserv
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A; Residues: 1-139 <GAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: S77052
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S77052
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                                                                                                                                                                                                                                                                                                   A;Gene: CESP:Y49E10.23
A;Map position: 3
A:Introns: 13/3; 59/2; 86/2; 141/3; 236/3; 267/3; 412/3; 480/1; 559/3; 628/2; 651/3; 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciraces: Or Mai-Zour sequence_revision U.T.Mai-Zour #text_cnange 31-Mai-Zour Ciracession: H96649

RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chio, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Maiziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID: 21016719
                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-734 <WIL>
A;Residues: 1-734 <WIL>
A;Cross-references: EMBL:Z98866; PIDN:CAB11567.1; GSPDB:GN00021; CESP:Y49E10.23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein F2401.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chloride channel protein homolog F9D12.10 - Arabidopsis thaliana CSpecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Peb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
C;Accession: T01843
R;Murray, J.; Langston, Y.; Ahrens, C.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of Arabidopsis thaliana F9D12.
A;Reference number: 214444
A;Reference number: 214444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 65;
3; Mismatches 6; Indels
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69;
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                         R;Barlow, K.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z20303
A;Accession: T27055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T01843
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                     A; Experimental source: clone Y49E10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 37.3%;
l Similarity 34.3%;
12; Conservative
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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Residues: 1-778 <STO>
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Accession: T27055
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Gaps

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Length 327;

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A; Cross-references strain B31
A; Experimental source: strain B31
C; Superfamily: unassigned APP-binding cassette proteins; ATP-binding cassette homolog C; Keywords: AFP; nucleotide binding; P-loop F; 23-214/Domain: ATP-binding cassette homology < ABC>F; 23-214/Domain: ATP-binding cassette homology of C; Keywords: ATP-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wnt-5c protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: 534173; 545242
R;Koster, J.G.; Kuiken, G.A.; Stegeman, B.; Peterson, J.; Eizema, K.; Stabel, L.; Dek
Submitted to the EMBL Data Library, June 1993
A;Description: Differential Xwnt-5C expression during early development of Xenopus la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson-Maduro, J.; Veenstra, G.J.C.; Koster, J.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spermidine/putrescine ABC transporter, ATP-binding protein (potA) homolog - Lyme dise C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Date: 13-Feb.1998 #sequence_revision 13-Feb.1998 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A70180
C; Accession: A70180
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943
A;Accession: A70180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
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44;
                                                                                                                                          DB 2;
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Pred. No. 42;
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Pred. No.
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Pred. No.
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C; Superfamily: int-1 transforming
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40.0%;
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Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                                                                                                  36.4%;
58.3%;
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                                                                                                                                                                                                                                                                                                          8 QQARNVQHYHKN 19
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Best Local Similarity
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A; Residues: 1-360 <KOS>
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-28 <KUI>
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A; Map position:
A; Introns: 231/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.; Ror
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable kinetechore (Skplp-like) protein At2g03190 [imported] - Arabidopsis thaliana N;Alternate names: SKpl-like protein T18E12.14 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar_1999 #sequence_revision 24-Mar_1999 #squence_revision 24-Mar_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: D84445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T02707; D84445
R; Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, September 1998
A; Description: A rabidopsis thaliana chromosome II BAC T18E12 genomic sequence. A; Reference number: 214702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o;
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A;Experimental source: strain Bristol N2; clone F57F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:93548811; PIDN:AAC34483.1; GSPDB:GN00139
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30079
F;Miller, N.; Bradshaw, H.
submitted to the EMBL Data Library, September 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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            F;21-139/Product: albumin 2S storage protein #status predicted <MAT>
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                                                                                                                          Length 139;
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A;Molecule type: DNA
A;Residues: 1-170 <ROU>
A;Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548811
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                        Indels
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                                                                                                                          Score 43; DB 2;
Pred. No. 16;
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illarity 47.6%; Pred. No. 20;
Conservative 2; Mismatches
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                                                                                                                          36.48;
66.78;
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                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                                                                                                                     4 DSCEQOARNVQH 15
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-170 <STO>
                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
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A; Status: preliminar
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Gaps

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Indels

Length 347;

PIDN:CAA51916.1; PID:9313268

Length 360;

Matches

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: CENP-C, an autoantigen in scleroderma, is a component of the human inner kin A;Reference number: A42681; MUID:92323541
       probable serine proteinase (EC 3.4.21.-) MLCB373.28 [similarity] - Mycobacterium lepr
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: A42681
R;Saitoh, H; Tomkiel, J.; Cooke, C.A.; Ratrie III, H.; Maurer, M.; Rothfiel
Cell 70, 115-125, 1992
A;Title: CENP-C, an autoantigen in scleroderma, is a component of the human
                                                   C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 06-Oct-2000
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C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C.Accession: C86026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                               C, Accession: T45448
R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: 222967
A;Accession: T45448
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: hydrolase; serine proteinase F;182,224,305/Active site: His, Asp, Ser #status predicted
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A;Experimental source: cosmid L373
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A;Map position: 4q12-4q13.3
C;Keywords: DNA binding; phosphoprotein
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129 NTPDSKKISSRNINDHH 145
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Matches 7; Conservative
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A; Residues: 1-943 <SAI>
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                                                                                                                                                                                                                                                                                                                                   adenylosuccinate lyase - Helicobacter pylori (strain J99)

C.Species: Helicobacter pylori

A.Variety: strain J99

C.Species: Helicobacter pylori

A.Variety: strain J99

C.Species: Train J99

C.Species: Larin J99

C.Speci
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R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Reference number: A64520; MUID:97394467
A; Accession: H64658
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD06609.1; PID:g415561
A;Experimental source: strain J99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenylosuccinate lyase - Helicobacter pylori (strain 26695)
C.Species: Helicobacter pylori
C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 22-Jun-1999
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               Indels
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54;
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Pred. No. 54;
6; Mismatches
       Mismatches
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                                                                                                                                               185 NFPKGSEEGARSLMNLQNNE 204
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                                                                           1 NSPDSCEQQARNVQHYHKNE
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Best Local Similarity 41.2*
Matches 7; Conservative
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RESULT T45448

C; Genetics

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A;Cross-references: GB:AE001863; GB:AE001825; NID:96460670; PIDN:AAF12411.1; PID:9646
A;Experimental source: strain R1
C;Genetics:
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hypothetical protein yieE [imported] -- Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Bete: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: D86056
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D86056
A;Status: preliminary
A;Accession: D86056
A;Accession: D86056
A;Accession: 1-562 - Ceno.
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A;Cross-references: GB:AE005174; NID:912518557; PIDN:AAG58912.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
A;Cross-references: GB:AE000448; GB:U00096; NID:g1790142; PIDN:AAC76735.1; PID:g17901
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yieE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Tile: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896 A;Reference number: A75574 A;Status: preliminary
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Pred. No. 50;
2; Mismatches
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Pred. No. 44;
5; Mismatches
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                                                                                                                                                                                                                                                                          Pred. No. 44;
5; Mismatches
                                                                                                                                                                                                                                              Score 42;
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35.3%;
                                                                                                                                                                                                                                       Query Match 35.6%;
Best Local Similarity 35.3%;
Matches 6; Conservative
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Matches 8; Conservative
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A; Residues: 1-288 <WHI>
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Best Local Similarity
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A; Residues: 1-1166 <BLAT>
A; Residues: 1-1166 <BLAT>
A; Cross-references: GB:AE000430; GB:U00096; NID:92367238; PIDN:AAC76555.1; PID:92367239;
A; Experimental source: strain K-12, substrain MG1655
R; Plunkett, G.
              A;Residues: 1-1002 <STO>
A;Cross-references: GB:AE005174; NID:912518248; PIDN:AAG58671.1; GSPDB:GN00145; UWGP:249
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: yhjt
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Molecule type: DNA
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                                                                                                                                                                                                                                                                       Length 1002;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U00039; NID:9466582; PID:9912469
                                                                                                                                                                                                                                                                   Score 42.5; DB 2;
Pred. No. 1.5e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1994 A; Reference number: S47666 A; Accession: S47751
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A; Residues: 1-602,'V',605-1166 <PLU>
                                                                                                                                                                                                                                                                                 36.0%;
55.6%;
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
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C;Accession: B81418
R;Parkhll, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil
C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72516.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A,Reference number: A81250; MUID:20150912
A,Accession: B81418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenylosuccinate lyase (EC 4.3.2.2) Cj0023 [imported] - Campylobacter jejuni (strain
                                                                                      C; percise; Caedion and all states are gains
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Sep-2000
C; Accession: T34467
R; Magdi, L.; Gattung, S.; Bartko, L.
Submitted to the EMBL Data Library, April 1997
R; Reference number: 221530
A; Reference number: 221530
A; Accession: T34467
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; References: EMBL: U97404; PIDN: AAB93310.1; GSPDB: GN00019; CESP: ZK770.3
A; Experimental source: strain Bristol N2; clone ZK770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Campylobacter jejuni
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein W02C12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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R;Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid W02C12.
                                                   nypothetical protein ZK770.3 · Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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C;Superfamily: fumarate hydratase
C;Keywords: amidine-lyase; carbon-nitrogen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
78;
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Pred. No. 78;
5; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
A;Introns: 43/2; 141/1; 202/3; 326/3
C;Superfamily: Passover protein
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41.2%;
                                                                            Species: Caenorhabditis elegans
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37.5%;
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232 SCEQIAVAIRHEQRTEV 248
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Best Local Similarity 3/...
6, Conservative
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Matches 7; Conserv
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A; Residues: 1-442 <PAR>
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T25934
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C;Species: Ambystoma mexicanum (axolotl)
C;Species: 21.01.1995 #sequence_revision 21.Jul-1995 #text_change 16-Jul-1999
C;Accession: B56549; S25000
R;Busse, U.; Seguin, C.
Mech. Dev. 40, 63-72, 1993
A;Title: Isolation of CDNAs for two closely related members of the axolotl Wnt family, A;Accession: B56549; WUID:93183769
                                                                                                                                                                               A;Residues: 1-295 <WAR>
A;Cross-references: EMBL:L41931; NID:g797276; PIDN:AAA68460.1; PID:g797277
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 214-271 <WA2>
Cross-references: EMBL:L42135; NID:g833750; PIDN:AAA68461.1; PID:g833751
Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: unassigned homeobox proteins; homeobox homology Keywords: DNA binding; homeobox; nucleus; transcription regulation 215-271/Domain: homeobox homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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A; Note: sequence extracted from NCBI backbone (NCBIP:126896)
C; Superfamily: int-1 transforming protein
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Mismatches
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40.0%; Pred. No. 0
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Pred. No.
                                                                                                                                                                   homeotic protein abd-A - Junonia coenia
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                                             232 DDAERFAAEVEHIHGNE 248
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Best Local Similarity 42.9
Matches 6; Conservative
DSCEQQARNVQHYHKNE
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Best Local Similarity
Matches 8; Conserva
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A;Molecule type: mRNA
A;Residues: 1-357 <BUS>
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A; Accession: S58851

Gene: abd-a

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A; Accession: 725934 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA

A; Residues: 1-498 <MUR>

A; Gene: CESP: W02C12.3

C; Genetics

A; Reference number: 220112

35.6%; Score 42; DB ilarity 50.0%; Pred. No. 89; Conservative 0; Mismatches

Best_Local Similarity
Matches 8; Conserv

Query Match

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Fixon de Bovenkamp, J.H.B.; Hau, C.M.; Strous, G.J.A.M.; Bueller, H.A.; Dekker, J.; E. Biochem. Biophys. Res. Commun. 245, 853-859, 1998
A;Title: Molecular cloning of human gastric mucin MUC5AC reveals conserved cysteine-r A;Reference number: JE0095; MUID:98249803
A;Reference number: JE0095
                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T46651
R;Bibbins, M.; Connerton, I.F.
submitted to the EMBL Data Library, March 1997
A;Description: Characterization of the regulator of acetate induction from N.Crassa.
A;Reference number: 223116
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C;Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 07-May-1999
C;Accession: JE0095
                                                                                                                                                                                                                                                                                                                                                                     C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 02-Sep-2000
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                    Length 816;
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C;Superfamily: GAL4 zinc binuclear cluster homology
F;19-56/Domain: GAL4 zinc binuclear cluster homology <GL4>
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;273-300/Domain: leucine zipper #status predicted <LZP>
                          Score 42; ...
Pred. No. 1.5e+02;
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Pred. No. 2.6e+02;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Y11565; PIDN:CAA72324.1
A;Experimental source: strain 74A (STA)
C;Genetics:
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                          Score 42;
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40.0%;
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43.8%;
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54.5%;
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A; Residues: 1-1373 <BOV>
A; Cross-references: GB: AF043909
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                                                                                  Conservative
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Best Local Similarity
Query Match
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521 EMTRNILHYHK 531
                                                                                                                                        QQARNVQHYHK 18
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C; Comment: The genome consists of two species of RNA, designated S (small) RNA and L (la C; Comment: Specific enzymatic cleavage may yield mature glycoproteins G1 and G2. However C; Superfamily: arenavirus surface glycoprotein
C; Superfamily: arenavirus surface glycoprotein
C; Keywords: glycoprotein
F; 67, 74, 89, 100, 111, 116, 121, 132, 181, 241, 379, 387, 404, 409, 499/Binding site: carbohydrate (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: 304149
R;Auperin, D.D.; Romanowski, V.; Galinski, M.; Bishop, D.H.L.
Y. Virol. 52, 897-904, 1984
A;Title: Sequencing studies of Pichinde arenavirus S RNA indicate a novel coding strateg
A;Reference number: A93005; WUID:85033957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84601
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                                                                                                                                              A;Cross-references: EMBL:U80815; PIDN:AAB37997.1; GSPDB:GN00022; CESP:W02C12.3 A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE002093; NID: 94567276; PIDN: AAD23689.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g21450 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface glycoprotein polyprotein - Pichinde virus
C;Species: Pichinde virus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 96/3; 128/3; 153/3; 196/3; 245/1; 270/2; 366/3; 417/1; 442/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.6%; Score 42; DB 1; Length 503,
                                                                                                                                                                                                                                                                                                                                                                           2; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 90; 2; Mismatches

44.48;

Best_Local Similarity 44.4 Matches 8; Conservative

Query Match

A; Molecule type: genomic RNA A; Residues: 1-503 <AUP>

1 NSPDSCEQQARNVQHYHK 18 81 NLPOSCSK -- NNTHHYYK 96

윱

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-816 <STO>

A; Map position:

C;Genetics:

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A;Reference number: A71800; MUID:99120557
A;Accession: C71875
A;Status: preliminary
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                                                                                                                                                                                                                                                           A; Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.99
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 42.9 tes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-337 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-463 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A;Map position: 2
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Bacies: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: D;Species: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3; 1d
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                                                                                                                                                                                                                                                                                                                       A; Modecule type: DNA
A; Residues: 1-3191 <WIL>
A; Cross-references: EMBL: 281094; PIDN: CAB03155.1; GSPDB:GN00023; CESP:T01D3.1
A; Experimental source: clone F58G11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:281110; PIDN:CAB03261.1; GSPDB:GN00023; CESP:T01D3.1 Experimental source: clone T01D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anther-specific protein TA-29 - common tobacco
C.Species: Nicotiana tabacum (common tobacco)
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.6%; Score 42; DB 2; Length 3191;
46.7%; Pred. No. 6.2e+02;
ive 1; Mismatches 7; Indels
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R; Seurinck, J.; Truettner, J.; Goldberg, R.B.
Nucleic Acids Res. 18, 3403, 1990
A; Title: The nucleotide sequence of an anther-specific gene.
A; Reference number: S13550; MUID:90287727
                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1996
A;Reference number: 219870
A;Accession: T24295
                                                                                                                                                         submitted to the EMBL Data Library, October 1996
A:Reference number: 219640
A:Accession: T22945
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                                                                                     C; Accession: T22945; T24295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-3191 <WI2>
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Best Local S
Matches 7
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hypotherical protein HP0948 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #text_change 28-Jul-2000
C;Accession: D64638
C;Accession: B64638
C;Accession: B64638
C;Accession: B64638
C;Accession: B64638
C;Accession: B64638
C;Accession: B64638
C;Accession: B66938
C;Accession: B66938
C;Accession: B64638
C;Acc
A;Molecule type: DNA ARN>
A;Residues: 1-337 ARN>
A;Cross-references: GB:AE001518; GB:AE001439; NID:g4155454; PIDN:AAD06466.1; PID:g415
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G849501
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
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C;Superfamily: Helicobacter pylori hypothetical protein HP0948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 337
                                                                                                                                                                                                                                                C;Genetics:
A;Gene: jhp0882
C;Superfamily: Helicobacter pylori hypothetical protein HP0948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.2%; Score 41.5; L
42.9%; Pred. No. 70;
:ive 4; Mismatches
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Wed Dec 19 08:45:39 2001

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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20263314
A;Accession: C83946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06090.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-205 GBLAE>
A; Residues: 1-205 GBLAE>
A; Cross-references: GB.BAE00242; GB.U00096; NID:91787720; PIDN:AAC74536.1; PID:917877
A; Experimental source: strain K-12, substrain MG1655
C; Superfamily: glutathione transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·;
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-Mar-2000
C;Accession: A64898
                                                                                                                                                                                                                             C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: C83946
                                                                                                                                                                                                                         hypothetical protein BH2371 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 50;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2;
Pred. No. 35;
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50.0%;
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118 APDAPEQLKKNVIEYRKS 135
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 50.0
Matches 7; Conservative
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                                            ||| :|: || :|:
23 PDSEQQKKRNKKHF 36
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A; Molecule type: DNA
A; Residues: 1-146 <STO>
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A,Experimental source: serogroup 01; strain N16961; biotype El Tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Du, Z.; Maggi, L.

Submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid K02D7.
A;Reference number: 221259
A;Accession: T32980
A;Accession: T32980
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-692 C00Z
A;Residues: 1-692 C00Z
A;Cross-references: EMBL:AF045645; PIDN:AAC02606.1; GSPDB:GN00022; CESP:T21D12.7
A;Experimental source: strain Bristol N2; clone K02D7
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A:Map position: 4
A:Introns: 29/1: 89/1: 127/1: 186/1: 233/1: 291/1: 379/3: 586/3: 611/3: 643/3
                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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45.0%; Pred. No. 1.5e+02;
tive 4; Mismatches 2; Indels
                    DB 2; Length 463;
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                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T21D12.7 - Caenorhabditis elegans
             Score 41.5; DE
Pred. No. 98;
1; Mismatches
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                    35.2%;
55.6%;
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A;Molecule type: DNA
A;Residues: 1-88 <HEI>
A;Cross-references: GB:AE004373;
                                                                                                                                                                                       391 NPDSCELQO---QDYIKN 405
                                                                                                                                               2 SPDSCEQQARNVQHYHKN 19
Ouery Match
Best Local Similarity 55.69
watches 10, Conservative
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les 9; Conserva
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A;Molecule type: DNA
A;Residues: 1-88 <HE2>
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Matches 7
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Search completed: December 17, 2001, 07:51:12 Job time: 94\ \mathrm{sec}
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N.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, N.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lerine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle N.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchl, M.; Tamakoshl, A.; Taraka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipters, M.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M.; Neference number sequence of the Gram-positive bacterium Bacillus subtilis.
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FEBS Lett. 303, 81-84, 1992
A;Title: Multiple genes for Xenopus activin receptor expressed during early embryogenesi
                                                      A; Molecule type: DNA
A; Residues: 1-229 <hr/>
A; Rossives: 1-229 <hr/>
A; Cross-references: GB:M23558; NID:g143497; PIDN:AAA22733.1; PID:g143499
A; Cross-references: GB:M23558; NID:g143497; PIDN:AAA22733.1; PID:g143499
B; Riust, F; Debarbouillie, M.; Maadek, T.; Young, M.; Mauel, C.; Karamata, D.; Klier, A. G. Bacteriol. 170, 5093-5101, 1988
A; Title: Deduced polypeptides encoded by the Bacillus subtilis sacU locus share homology A; Reference number: A30190; MUD:89033890
A; Accession: B30190
A; Molecule type: DNA
A; Residues: 1-229 <KUN>
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A;Experimental source: strain 168
C;Comment: This protein has two functional regions: the amino-terminal region, which con which carries the enhancing activity for these enzymes.
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A;Start codon: GTG
S:Superfamily: regulatory protein comA; response regulator homology
C;Keywords: DNA binding; phosphoprotein; transcription regulation; two-component regulat
F;6-117/Domain: response regulator homology <RRH>
F;56/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tanaka, T.; Kawata, M.
J. Bacteriol. 170, 3593-3600, 1988
A;Title: Cloning and characterization of Bacillus subtilis iep, which has positive and
A;Reference number: A31097; WUID:88298669
A;Accession: A31097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 28-Feb-1997
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A;Cross-references: GB:M21658; NID:g143087; PIDN:AAA22545.1; PID:g143089
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: M23649; NID: 9143500; PIDN: AAA22735.1; PID: 9143502
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Pred. No. 56;
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A; Reference number: A30191; MUID: 89033891
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50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C;Accession: S39484
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A;Molecule type: mRNA
A;Residues: 1-575 <KUH>
A;Residues: 1-575 <KUH>
C;Keywords: DNA binding
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                                                                                                                                                                                            Length 512;
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Pred. No. 1.56+02;
7; Indels
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                       A; Accession: S21171
A; Molecule type: mRNA
A; Residues: 1-512 <NIS>
C; Superfamily: activin receptor II; protein kinase homology
C; Keywords: ATP
F; 189-485/Domain: protein kinase homology <KIN>
                                                                                                                                                                            Score 41; DB 2; Ler
Pred. No. 1.3e+02;
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A;Title: DNA binding factor GT-2 from Arabidopsis. A;Reference number: S39484; MUID:94033312
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                                                                                                                                                                                                                                          2; Mismatches
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A; Reference number: S21171; MUID: 92275088
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Best Local Similarity 41.7%;
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41.28;
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65.249 Million cell updates/sec
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/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 150 summaries
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1 NSPDSCEQQARNVQHYHKNEL 21
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Gapop 10.0 , Gapext 0.5
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Perfect :
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Mouse tag7 clone p Human tag7 clone p Human PR01269 prot Htag7 protein enco Chondrosarcoma pep Human PR01269 (UNQ Protein of the inv Human 5' EST relat Bovine granulocyte Human ORFX ORF2895 Murine granulocyte Description SUMMARIES AAB24022 AAB25583 AAY96964 AAY99400 AAB66149 AAY64935 AAW23722 AAB43131 AAW23723 AAY00770 AAY 00771 Query Match Length DB 181 182 196 196 196 196 196 196 190 400 86 86 86 86 77 73 46 Result è

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Gaps

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Indels

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1 NSPDSCEQQARNVQHYHKNEL

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RESULT 2 AAY00770 ID AAY00770 standard; Protein; 182 AA.

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AAX84440
                        AAY94961
                  AAB54316
         AAG13666
 AAW98845
          AAW8627
       AAB47
38.5
38.5
38
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Human pancreatic c Human colon cancer Peptide #7528 enco Peptide #11330 enc lysosomal si ena/VASP-lik ena/VASP-lik Signal transduction Human PRO864 prote Human PRO864 (UNO4 Wnt-4AF and Wnt-5c Wnt-4AF and Wnt-5c Wnt-4AF and Wnt-5c prote Human 36PlA6 trans Human pancreatic c Fission yeast STE2 Mouse asthlj prote Mouse asthlj prote Staphylococcus xyl Rat bone formation D.melanogaster cor Transgenic mouse N Human ASTHlJ prote Human 36PlA6 trans B Streptococ ORFX ORF2042 cytoskeleton ORFX ORF2399 D.melanogaster cor protein sequ secreted pro Amino acid sequenc Human polypeptide Human ORFX ORF1356 PN7771, Homo sapi Core polypeptide T Core polypeptide f Arabidopsis thalia Human scaffold att Blastx output of h Human secreted pro Human endometrium Arabidopsis thalia Protein which is s Human breast tumou Human prostate can Human colon cancer Arabidopsis thalia Human colon cancer Human colon cancer Human GAK protein Protein kinase GAK Human cancer assoc H. pylori GHPO 158 Human ATP-dependen Human protein sequ Human polypeptide Amino acid sequenc Photorhabdus lumin Arabidopsis thalia Arabidopsis thalia Human polypeptide Human polypeptide Human ORFX ORF318 Core polypeptide Human ASTHLJ Group 1 Human (Human Нишап Human Human Human Human

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This protein comprises the precursor of a novel, claimed antimicrobial peptide from murine neutrophils, designated murine antimicrobial peptide from murine neutrophils, designated murine coramic adduced from a cDNA clone (see AAR78510) obtained from murine bone marrow. MGP-A and the bovine homologue, BGP-A (see AAW2724), exhibit activity against Gram-positive and Gram-regative AAW2724), exhibit activity against Gram-positive and Gram-regative Escherichia coli, Candida albicans, Salmonella typhimurium and C. candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary in properticularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity. Carboxamidated analogues of MGP-A and BGP-A may also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                         Location/Qualifiers
170..181
/label= Mat_peptide
/note= "MGP-A antimicrobial peptide (Claim 3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 181;
                                                                                                                                Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis;
                                                                                                 Murine granulocyte peptide A precursor (antimicrobial MGP-A).
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AAW23723 standard; Protein; 181 AA.
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                                                                       (first entry)
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N-PSDB; AAT78510.
                                                                                                                                                                                                endotoxaemia; mouse.
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                                                                       18-FEB-1998
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                                      AAW23723;
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Peptide
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Prokhorchouk E;

Mus sp.

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This sequence is the human tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumnours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; sa an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 86; DB 20; Length 191; 71.4%; Pred. No. 2.9e-06; Live 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 126-127; 138pp; English.
                                                                                                                                                                                                                         Ostermann E,
                                                                                                                                                                              BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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N-PSDB; AAX21820.
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Matches 15; Conserv
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identification;
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01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the murine tag? of the invention. Cells containing the tag? DNA sequence are used to express recombinant tag? Tag? Is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver. ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), asrcoma (Kaposi's, osteo or fibro-sarcomas), melanoma or teratocarcinoma), asrcoma docular weight marker. The tag? polypeptide inhibits tumour growth and induces apoptosis. The tag? coding sequences are also useful as probes for gene mapping and detection of tag? gene expression, and as probes for gene against tag? are used as reagents for detecting tag?; as an antagonist of tag?; for isolating tag? and therapeutically to inhibit or delay tumour
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                                                                                                                                            inhibitor; mammalian tumour; carcinoma; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding tag? - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostermann E, Prokhorchouk E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 20;
Pred. No. 1.6e-11;
; Mismatches 0;
                                                                                                                                                                 melanoma; leukaemia; apoptosis inducer; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                  (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY00771 standard; Protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tag7 clone protein sequence
                                                                                                   Mouse tag7 clone protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Fig 1; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                         97US-0893764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1999 (first entry)
                                                          18-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kiselev S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-120887/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX21819
                                                                                                                                                                                                                                                 WO9902686-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                         11-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georgiev G,
                                                                                                                                                                                                                                                                                          21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY00771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps

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proliferation; cancer;

AXX00771 1D AAY0 XX AC AAYC XX IB-P XX IB-P

Wood WI;

Watanabe CK,

Roy MA,

Gurney AL,

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The present invention describes an antibody that binds to a human protein (I) selected from: PRO181; PRO1269; PRO1410; PRO1755; PRO1780; PRO344; PRO1957; PRO1955; PRO1959; PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; inflammatory disorder; inflammatory bowel disease; croin's disease; nephritis; hyperproliferative disorder; cancer; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                                                                                                                                                     Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Htag7 protein encoded by human secreted protein gene #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanoma; lymphoma; wound healing; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB25583 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                         claim 61; Fig 4; 226pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSPDSCEQOARNVQHYHKNEL
99WO-US28634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4
Matches 15; Conservative
                                                                                                     3otstein D, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
                                                      (GETH ) GENENTECH INC
                                                                                                                                                         WPI; 2000-594320/56.
N-PSDB; AAC58104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2000
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01-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB25583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in AAA80666-A80623 encode the 12 secreted proteins agiven in expensive in which they are expressed. Examples of the control they are expressed. Examples of the control they are include: immunosuppressant; activities of the proteins include: intrarteriosclerotic; antichners; vulnerary; antiarteriosclerotic; antichners; vulnerary; antiarteriosclerotic; antichners; vulnerary; antiarteriosclerotic; antichners; vulnerary; antiarteriosclerotic; antichners; vulnerary; contriviral; antiarteriosclerotic; and conditions examples of and/or diagnose various disease, disorders and conditions examples of and/or diagnose various disease, disorders and conditions examples of arthritis, dermatitis, and multiple sclerosis; inflammatory disorders such as paraporoteinaemias and purpura; cardiovascular disorders such as paraporoteinaemias and purpura; cardiovascular disorders such as paraporoteinaemias and purpura; cardiovascular disorders such as paraporoteins and polynucleotide cancer e.g. melanoma and lymphoma. The proteins and polynucleotide cancer e.g. melanoma and lymphoma. The proteins and polynucleotide cancer e.g. melanoma and lymphoma. The proteins and shallofolide sequences are represented in sequences AAA806613 and AAB25583. Sequences are represent genes related to the secreted protein genef8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; regulator; chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data.
                                                                                                                                                       Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                          Wei Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                        Olsen HS, Young PE, Kenny JJ, Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 86; DB 21.71.4%; Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96964 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                 Claim 1; Figure 34; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2000 (first entry)
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/label= N
34..117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                              WPI; 2000-387742/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 AA;
                                                       Ruben SM,
                                                                                                                                  N-PSDB; AAA80613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY96964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                           Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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Gaps

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4; Indels

Score 86; DB 21; Pred. No. 3e-06; 2; Mismatches 4;

72.98; 71.48;

21

98US-0105971.

Length 196;

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Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
    Human PRO1269 (UN0639) amino acid sequence SEQ ID NO:216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9805-0101068.
9805-0101071.
9805-0101279.
9805-0101471.
9805-0101474.
9805-0101477.
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98US-0102487.
98US-0102570.
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980S-0100930.
980S-0100848.
980S-0100849.
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98US-0099642.
98US-0099741.
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98US-0100388.
98US-0100390.
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98US-0100710.
98US-0100711.
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98US-0099596.
98US-0099598.
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98US-0099808.
98US-0099812.
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98US-0101915
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98US-0099763
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98US-0099816
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                                                                                                                  99WO-US20111
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                                                                           WO200012708-A2.
                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-SEP-1998
                                                                                                                    01-SEP-1999;
                                                                                                                                                                                                                      09-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-C), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DRA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (Clalmed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against
                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TNF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 86; DB 21; Length 196; 71.4%; Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3e-(; Mismatches
                                                                                                                                                                                                                                                                                                       Olsen HS;
                                                                                                                                                168..181
/label- Antigenic_region
190..196
                                                                                                                                                                       190..196
/label- Antigenic_region
                                                                                                   Antigenic_region
                                                                                                                      Antigenic_region
                                                                                                                                          Antigenic_region
 /label- PGRP-like_domain
                     label= Antigenic_region
                              .0..29
'label- Antigenic_region
                                                   3..43
label- Antigenic_region
                                                                     63..79
/label- Antigenic_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY99400 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 3; 191pp; English
                                                                                                                                                                                                                                                                                                       Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.9%;
Best Local Similarity 71.4%;
Matches 15; Conservative
                                                                                                                                                                                                                                           99WO-US30736.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                          133..146
/label- An
                                                                                                                                160..165
/label= A
                                                                                        99..112
/label-
                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                         WPI; 2000-452414/39.
N-PSDB; AAA51719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 AA;
                                                                                                                                                                                                     WO200039327-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2000
                                                                                                                                                                                                                                                               23-DEC-1998;
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                                                                                                                                                                                                                        06-JUL-2000
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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
                                               AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent pCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to secreted and transmembrane proteins.
small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fong S;
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton DL, Ferrara N,
maldi CJ, Gurney AL,
Stewart TA, Tumas D;
                                                                                                                                                                                                                   Score 86; DB 21; Length 196;
Pred. No. 3e-06;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker KP, Botstein D, Desnoyers L, Eaton DL
Gao W, Goddard A, Godowski PJ, Grimaldi CJ,
Pan J, Paoni NF, Roy MA, Smith V, Stewart
Patanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted; transmembrane; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                    AAB66149 standard; protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 122; 787pp; English.
                             Claim 12; Fig 122; 773pp; English.
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99WO-US28551.
99WO-US30095.
2000WO-US00219.
                                                                                                                                                                                                                         72.9%;
milarity 71.4%;
Conservative 2
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99US-0145698.
99WO-US20111.
99US-0162506.
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                                                                                                                                                                                                                                                                             1 NSPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                                                                                            68 ntpascqqqarnvqhyhmktl
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Pan J, Paoni NF, Roy
Watanabe CK, Williams
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                          196 AA;
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06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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              New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or
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980S-0105881.
980S-0105882.
980S-0106062.
980S-0106029.
980S-0106030.
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98US-0106464.
98US-0106856.
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980S-0105104.
980S-0105169.
980S-0105266.
980S-0105693.
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98US-0106248.
98US-0106384.
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98US-0108852
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98US-0103258.
98US-0103449.
98US-0103314.
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98US-0103678
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29-0CT-1998;
29-0CT-1998;
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06-0CT-1998;
07-0CT-1998;
07-0CT-1998;
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07-OCT-1998;
08-OCT-1998;
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08-OCT-19
14-OCT-19
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20-0CT-19
20-0CT-19
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AAY6438 represent the EST-related proteins. AAX64651 to AAX4305. The S' ESTs can be used for producing secreted human gene products. The S' ESTs can be used for producing secreted human gene products. They can be used for producing secreted human gene regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in also be used in forensic procedures to identify individuals, or in gene therapy protocols. The nucleic acids encoding signal peptides can used for directing extracellular secretion of a polypeptide or the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in
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                             probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents.
   These proteins and the DNA encoding them may be used as hybridization
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                            3e-06;
                                                                                                                                                      The nucleic acids may also be used in gene therapy
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                                                                                                                                                                                                                                                                                                        Score 86; DB 2
Pred. No. 3e-06
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY64935 standard; Protein; 116 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NSPDSCEQQARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                            72.98;
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Matches 15; Conservative
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N-PSDB; AAZ42549.
                                                                                                                                                                                                                    196 AA;
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treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW23725), exhibit activity against Gram-positive and Gram-negative bacteria, fungi and viruses, specifically Staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
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                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; bovine granulocyte peptide A; BGP-A; preservative; sepsis;
                                                                                                                                                                                                                                                                                                                                                      Bovine granulocyte peptide A precursor (antimicrobial BGP-A).
                                                                                                              Length 116;
                                                                                                     Score 77; DB 21; Length 11.
Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label = Sig_peptide
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/label- Mat_peptide
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/label= Propeptide
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                                                                                                               65.3%;
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                                                                                                                                                                                        (first entry)
                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   endotoxaemia; cattle
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                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                          116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; hepatotropic;
                                                                                                                                                                                                                                 Gaps
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medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity. Carboxamidated analogues of BGP-A and MGP-A may also be used.
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                                                                                                                                                                                            Length 190;
                                                                                                                                                                                            Score 73; DB 18; Length 19
Pred. No. 0.00038;
; Mismatches 3; Indels
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neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                open reading frame; ORFX; detection;
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                              Query Match 61.9%;
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive
                                                                                                                                                                                                                                                                     1 NSPDSCEQOARNVQHYHKNE
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                                                                                                                                                  190 AA;
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                                                                                                                                                    Sequence
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides novel human stem cell growth factor-like
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                                                                                                                                                                                                    21; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mize NK,
                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee J,
                                                                                                                                                                                                                                                                                                                                                   Tumour endothelial marker 7 precursor protein.
                                                                                                                                                                                                    Score 46; DB 2
Pred. No. 23;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 149-150; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                  AAB85400 standard; Protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Drmanac RT,
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294 spdvpesrrrsifeyhriel 313
                                                                                                                                                                                                       39.0%;
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2000US-0545714.
2000US-0547358.
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                         2 SPDSCEQQARNVQHYHKNEL
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200153500-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-2000;
11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Labat I,
                                                                                                                                                                                                                                                                                                                     AAB85400;
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                    12
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          888888888888888888888888
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helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 cys2His2, CCAAT box elements and MYB.

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Gaps

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Indels

8

3; Mismatches

10; Conservative

Query Match Best Local Similarity Matches 10; Conserv

Length 214;

Score 45.5; DB 21; Pred. No. 14;

38.6%;

214 AA;

Sequence

8X888

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polypeptides and polynucleotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polynucleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be used of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothelial marker of precursor protein, homologous to a stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeocitic; homeociomain; homeociox; MADS; homeociomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                                                                                                 22; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pinus radiata transcription factor protein sequence #166.
                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                 Score 46; DB
Pred. No. 25;
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                              AAB33039 standard; Protein; 214 AA.
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195 spdvpesrrrsifeyhriel 214
                                                                                                                                                                                                39.0%;
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99US-0149485.
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                    Query Match
Best Local Similarity
'-has 9; Conserv?
                                                                                                                                                           431 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus radiata
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18-AUG-1999;
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                                                                                                                                 polypeptide
                                                                                                                                                             Seguence
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Gaps

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The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide 8; Page 403; 747pp; English. WPI; 2000-579369/54 Claim

Glenn M;

Shenk MA,

Wood M, McGrath A,

(GENE-) GENESIS RES & DEV CORP LTD. (FLET-) FLETCHER CHALLENGE FORESTS LTD.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the human Rab protein D (HRABD) encoded by the HRABD CDNA which was first identified in CDNA Incyte clone 358844 from the synovial tissue cDNA ilbrary SYNORABOL. The invention also claims for other human Rab protein (HRAB) CDNAs and the HRAB proteins they encode, namely HRABA (AAV32008, AAW42095). HRABB (AAV32009, AAW42095) and HRABC (AAV32010, AAW42097). The Rab proteins are claimed to be involved in the regulation of intracellular vesicular transport in both exocytic and endocytic pathways. As Rab proteins play a role in mediating the function of a viral gene, Rev, which is essential for replication of HIV-1 and as they also mediate cell cycle events, the present Rab proteins are claimed to be useful in the diagnosis, prevention, or treatment of choroideremia, AIDS and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                     Human Rab protein D; HRABD; HRABA; HRABB; HRABB; Rev; HIV-1; intracellular vesicular transport; choroideremia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human Rab protein(s) - used to develop products for diagnosis, prevention and treatment of choroideremia, AIDS and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                      AAW42098 standard; Protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 58; Fig 4A-4B; 88pp; English.
               1 NSPDSCEQ---QARNVQHYHKNEL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.1%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                            97WO-US18581.
                                                                                                                                                                                             Human Rab protein D (HRABD).
                                                                                                                                                                                                                                                                                                                                                                                                        96US-0741411
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                         exocytosis; endocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-272232/24.
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                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1997;
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                                                                                                                                                                 23-SEP-1998
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                                                                                                                                     AAW42098;
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Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
Human secreted protein encoded by gene 75 clone HBIAB39.
                                                                  Location/Qualifiers
108
                                                                                             /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0047588.
97US-0047589.
97US-0047590.
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970S-0047594.
970S-0047595.
970S-0047596.
970S-0047597.
970S-0047598.
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97US-0047632
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                                                                                                                                                    98WO-US04493
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97US-0040334
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970S-00475
970S-00475
970S-00475
970S-00475
                                                                                    Misc-difference
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                                                                                                                                                     06-MAR-1998;
                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP: see A131315-A4157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                     Peptide #8322 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 22; Length 33;
Pred. No. 2.8;
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                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 34554; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW74953 standard; Protein; 108 AA.
                                                                                  AAM34285 standard; Protein; 33 AA.
                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                     26 MAX-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-MUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%;
40.0%;
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3 apqpceqqahpvdrwwerev 22
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                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                            2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1999 (first entry)
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Best Local Similarity 40.0°
Matches 8; Conservative
                                                                                                                      17-OCT-2001 (first entry)
                             escasavrnveyygsn 76
                 DSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                                                                                                                                                    genetic disorder
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                                                                                                                                                                                      Homo sapiens.
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                                                                                                    AAM34285;
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AAW74953
ID AAW7499
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AC AAW7499
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Claim 1; Page 671; 721pp; English.
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Feng P. Ferrie AM, Fischer CI
Kyaw H, Lafleur DW, Li Y, Mc
Ruben SM, Shi Y, Soppet DR,
                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                    97US-0056664
97US-0056845
                                                                                                                                   97US-0056876
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970S-0056880
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97US-0056886
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97US-0058785
97US-0047633
97US-0048964
                    97US-0049610
                         97US-0051926
                                       97US-0055724
97US-0056630
                                                          97US-0056632
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97US-0056874
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N-PSDB; AAV59738.
                         08-JUL-1997
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Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA; Feng P, Ferrite AM, Fischer CL, Florence KA, Greene JM, Hu JS; Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;

encode New isolated human genes and the secreted polypeptide(s) they enco - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 75 from the human cDNA clone HBIAB39 (deposited as clone ATCC 97900 and ATCC 209046).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Pc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in

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amino acid sequences with which they share homology. The genes and proteins have activities dependent on the tissues and cells in which they proteins have activities dependent on the tissues and cells in which they care expressed. Examples of their activities include cytostatic; are expressed. Examples of their activities include cytostatic; municosuppressive; mootropic; neuroprotective; antiviral; antiallargic; hepatotropic; antidabetts; antifungal; antiparasitic; and cardiant. The secreted proteins, polypeptides, antigonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as cancer, particularly breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, unuy, or urogenital. Immune disorders such as Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as
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the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequences AAC95521 - AAC95570 represent cDNA encoding 50 human secreted proteins AAB52012 - AAB52161. Sequences AAB52062 - AAB52103 represent alternative polypeptides encoded by the genes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprofective, antiviral; antiallergic; hepitotropic; antidiabetic; antinflammatory; antiuleer; vulnerary; antionvulsant; antibocterial; antifungal; antiparasitic; cardiant; cancer; immune disease; allergy; cardiovascular disorder; wound healing; infection; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 27 human secreted protein homologous amino acid sequence #132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; cytostatic; immunosuppressive; nootropic;
                                                                                                                                                                                       ;
0
                                                                                                                                            Score 44; DB 19; Length 108; Pred. No. 11;
                                                                                                                                                                                         Indels
                                                                                                                                                                                         7;
                                                                                                                                                                                           5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                AAB52083 standard; Protein; 183 AA.
                                                                                                                                                37.3%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMA-) HUMAN GENOME SCI INC
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20-JAN-2000; 2000US-0176068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000; 2000WO-US08983
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59 nlgelcgrlvrnveyygsn 77
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                                                                                                                                                     Query Match 37.3
Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM, Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-611865/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                         108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAB52083;
                                                                                             Sequence
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polynucleotide sequences AAC95521 - AAC95570 represent cDNA encoding 50 human secreted proteins AAB52012 - AAB52161. Sequences AAB52062 - AAB52103 represent alternative polypeptides encoded by the genes, and amino acid sequences with which they share homology. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include cytostatic; hemourosuppressive, noctropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antilinflammatory; antivical; vulnerary; anticonvulsant; antibacterial; antifungal; antipores; vulnerary; anticonvulsant; antibacterial; antifungal; antiposis and agonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as cancer, particularly breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract,
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; cancer; immune disease; allergy; cardiovascular disorder; wound healing; infection; neurological disease.
myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and infectious diseases such as viral, bacterial, fungal and parasitic infections may also be treated using the proteins and polynucleotides of the invention. Sequences AAC95512 - AAC95520 and AAB52011 are used in the isolation and characterisation of the proteins and polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; cytostatic; immunosuppressive; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein sequence encoded by gene 27 SEQ ID NO:133.
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                                                                                                                                                                                     Score 44; DB 21; Length 183;
Pred. No. 20;
5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAB52084 standard; Protein; 183 AA
                                                                                                                                                                                             37.3%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-2000; 2000US-0176068.
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                                                                                                                                                                                                                                                                           1 NSPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                57 nvqelcqrlvrnveyyqsn 75
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                                                                                                                                                                           Ouery Match
Best Local Similarity 30...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-611865/58.
                                                                                                                                          183 AA;
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                                                                                                                                          Sequence
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This invention describes a novel isolated and purified polynucleotide sequence (I) of 802 base pairs encoding the human Rab-specific guanine-nucleotide dissociation inhibitor (RGDI) polypeptide (II). The protein described in the method of the invention has anti-HIV: The antineurodegenerative, anti-isohemic, antianemic, vasotropic, recombinant production of RGDI, in gene therapy, including expression of complements of (I), as a source of antisense, triplex forming or ribozyme therapeutics, as a source of probes and primers for diagnosis and monitoring of RGDI-related diseases, in usual amplification and/or
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGDI; Rab-specific guanine-nucleotide dissociation inhibitor; anti-HIV; antineurodegenerative; anti-ischemic; antianemic; vasotropic; detection; hepatotropic; cytostatic; anti-inflammatory; gene therapy; apoptosis; acquired immune deficiency syndrome; neurodegeneration; aplaatic anemia; retinitis pigmentosa; ischemic injury; cirrhosis; cancer; inflammation; allergy; Crohn's disease; multiple sclerosis; diagnosis.
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allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allabetes meallitus, Crohn's disease, multiple sclerosis. Theumatoid arthritis and ulcerative collitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as myocardial anoxia and epilepsy; and infectious diseases such as viral, bacterial, fungal and parasitic infections may also be treated using the proteins and polynucleotides of the invention. Sequences AAC95512.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nucleic acid encoding guanine-nucleotide dissociation inhibitor, used for diagnosis, treatment and prevention of abnormal apoptosis such as neurodegeneration or cancer
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                                                                                                                                                                                                                                               Score 44; DB 21; Length 183;
Pred. No. 20;
5; Mismatches 7; Indels
                                                                                                                                                             the proteins and polynucleotides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51559 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                     37.3%;
36.8%;
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Best Local Similarity 36.8.
----- 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RGDI protein
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9705-005684.
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970S-0056876.
970S-0056877.
970S-0056878.
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970S-0047632.
970S-0047633.
970S-0048974.
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970S-0048974.
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97US-0047583.
97US-0047584.
97US-0047584.
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97US-0047590.
97US-0047592.
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97US-0047596.
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97US-0047613.
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97US-0047617.
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970S-0055724
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22-AUG-1997
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23-MAY-1997;
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hybridization tests, for genomic mapping and for detecting mutations. RGDI is used to treat or prevent disorders associated with increased apoptosis, e.g. acquired immune deficiency syndrome, neurodegenration, retinitis pigmentosa, aplastic anemia, ischemic injuries, and cirrhosis. RGDI is used to raise specific antibodies (Ab) or to screen for specific antagonists and agonists which are potential therapeutic agents. Antagonists of RGDI are used to treat abnormal cellular proliferation, e.g. many forms of cancer and inflammation such as allergy, Crohn's disease and multiple sclerosis. Ab are used as therapeutic antagonists disease and multiple sclerosis. Ab are used as therapeutic antagonists RGDI-related diseases, in competitive drugs), to diagnose and monitor from natural sources. This sequence represents the human RGDI protein described in the method of the invention.
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.
                                                                                                                                                                                                             Score 44; DB 21; Length 185;
Pred. No. 20;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein encoded by gene 75 clone HBIAB39.
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186
                                                                                                                                                                                                                                                                                                                                                    AAW74804 standard; Protein; 186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label- unknown
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970S-0040161.
970S-0040163.
970S-0040333.
970S-0040334.
970S-0040336.
970S-0040336.
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97US-0043670.
97US-0043671.
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36.8%;
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59 nlgelcqrlvrnveyyqsn 77
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Best Local Similarity 36.07
Conservative
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07-MAR-1997;
07-MAR-1997;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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WO200134643-A1.

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This sequence represents a secreted human protein encoded by the nucleic acid molecule designated Gene 75 from the human cDNA clone HBIAB39 (deposited as clone ATCC 97900 and ATCC 209046).

The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 186 the new polymucleotides. Specific uses are described for each of the 186 the new polymucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                     Endress GA;
                                                                                                                                                                                                                                                                                    Hu JS;
Rosen CA;
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                                                                                                                                                                                                                                                                                       Greene JM,
                                                                                                                                                                                                                                                     LA, Carter KC, Duan R, Ebner R, I
Fischer CL, Florence KA, Greene JM
Li Y, Moore PA, Ni J, Olsen HS,
oppet DR, Young PE, Yu GL, Zeng Z;
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Kyaw H, Lafleur DW, Li Y, M
Ruben SM, Shi Y, Soppet DR,
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36.8%;
                              97US-0057650.
97US-0057669.
97US-0057761.
97US-0058785.
                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NSPDSCEQQARNVQHYHKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 nlgelcgrlvrnveyygsn 77
   97us-0056911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                   Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-506364/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV59585
                                                                                                                                                                                                                                                                   Bednarik DP,
22-AUG-1997
05-SEP-1997
                                                                                               05-SEP-1997
                                                                05-SEP-1997
                                                                                                                                 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE04179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AC AAE0
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AADO8404-AADO8478 represent cDNAS corresponding to 24 human secreted protein genes, and AAE04170-AAE04170 represent the protein fragments of the secreted proteins they encode. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

Cor ameliorating medical conditions, e.g., by protein or gene therapy. Cor ameliorating medical conditions and be diagnosed by determining the amount of the pathological conditions can be diagnosed by determining the amount of the correction in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, the new genes. Specific uses are described for each of the 24 genes, the new genes. Specific uses are described for each of the 24 genes, correctly cancer, tumours, foetal and developmental abnormalities, discaders, cancer, tumours, discases of the immune system, AIDS, autoimmune conditive disorders (e.g., Alzheimer's discase, Parkinson's disease), conditive disorders, cantantials, sepsis, diabetes, atherosclerosis, cardiovascular disorders, conditive disorders, and decental disorders, and downd healing and epithalial cell or proteins can also be used to aid wound healing and epithalial cell conference tissues, to identify their cognate ligands or binding to partners, and in chemotaxis, and can be used as a food additive or preserved the amount of preserved to modify storders. An allowascular disorders or preserved to modify storders and in chemotaxis, and compare injamics or binding to partners, and in chemotaxis, and the used as a food additive or preserved to modify storders and in chemotaxis, and the used as a food additive or preserved to an another or an analysis of the partners and in chemotaxis, and the partners and in chemotaxis, and in allowable in the partners and in chemotaxis, and in a partners and in chemotaxis, and in allowable in the partners and in chemotaxis, and in chemotaxis, and in chemotaxis, and in chemotaxis, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                             Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                             Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus capitis FemA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY08218 standard; Protein; 427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 13; 532pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%;
38.9%;
                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                               12-NOV-1999; 99US-0164825.
03-AUG-2000; 2000US-0222904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PDSCEQQARNVQHYHKNE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ppgcrnsargeghyhhgd 28
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                                                                                   08-NOV-2000; 2000WO-US30629
                                                                                                                                                                                                                                                  Ruben SM, Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 38.9 nes 7; Conservative
                                                                                                                                                                                                                                                                                                 WPI; 2001-374441/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 AA;
                                         17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY08218;
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BX BX SX B
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Homo sapiens

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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressant; artidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes of different Staphylococci species or other gram-positive bacteria. The femA nucleic acids can also be used in therapeutic applications. They can also be used to identify inhibitors, e.g. antibodies or antisense oligonucleotides, for blocking expression of the femA nucleotide sequences. They can also be used for producing vaccines against Staphylococci infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based on the consensus feam nucleotide sequence which are used to develop products for the identification, detection and therapy of infections. The oligonucleotides can be used for the genetic amplification, the identification and/or quantification of various fema sequences which are specific to known or unknown Staphylococi species. Since the fema sequence is similar to the fema sequence, the oligonucleotides can also be used for the molecular genotyping of femB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel Staphylococcus-specific oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.3%; Score 44; DB 20; Length 427; 35.5%; Pred. No. 53;
                FemA; identification; detection; therapy; infection; femB; amplification; genotyping; gram-positive bacteria; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF439 polypeptide sequence SEQ ID NO:878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus-specific oligonucleotides
                                                                                                                                    /note= "in frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NSPDSCEQQ-----ARNVQHYHKNEL 21
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Fig 9a-b; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB40675 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                     DEFENCE
                                                                                                                                                                                                                                                                                  97EP-0870146.
                                                                                                                                                                                                                                               98WO-BE00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                   (BENA-) BELGIAN MIN NAT (UYLO-) UNIV CATHOLIQUE
                                                                    Staphylococcus capitis
                                                                                                                                                                                                                                                                                                                                                                        Sala J, Vannuffel P;
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-287521/24.
                                                                                                                     Misc-difference 412
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX37801
                                                                                                                                                                           W09916780-A2
                                                                                                                                                                                                                                               28-SEP-1998;
                                                                                                                                                                                                                                                                                  26-SEP-1997;
                                                                                                                                                                                                              08-APR-1999
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Gaps

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ANCHAAD TO ARAL/PUD ENCOUE THE PROTECTING 91/04-01. TO ARAL/S27,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
caquences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
csteophathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiflammatory; antibacterial; antiviral; antifleumatic;
antidiflammatory; antibacterial; antiviral; antifleumatic;
antithyroid; and antidanemic. The sequences can be used for determining
the presence of or predisposition to, or preventing or treating
pathological conditions associated with an ORFX-associated disorder. The
nucleic acids can be used to express ORFX proteins in gene therapy
vectors: The proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
grafit vs host disease, cardiovascular disease; diabetes mellitus,
cythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
bacterial or fungal infection, malaria, autoimmune disorders, asthma,
allergies, aplastic aneemia, burns, wounds, bone and cartilage damage,
nocturnal haemoglobinuria, antiinfilammatory disease; to enhance
coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinutia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frame X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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42.9%; Pred. No. 25;
tive 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 900; 5507pp; English
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                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621
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    6 CEQQARNVQHYHKN 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 ceeeaqavreyhqd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC74884
                                                                                                                                                                                                                                                 WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                           Homo sapiens.
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ID AAG9
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, Coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium in the useful for producing amino acids, nucleic acids, vitemins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum; carbon metabolism and energy production;
                                                                                                                                                                                                                                                                                                                                                                                  Ando S, Hayashi M, Ochiai K, Yokoi H;
da M, Ozaki A;
                                                                                               Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum SMP protein sequence SEQ ID NO:414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO: 6407; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 384;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                              C glutamicum protein fragment SEQ ID NO: 6407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB :
Pred. No. 69;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB79449 standard; Protein; 388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.4%;
                                                                                                                                                                                                                                                                                    16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                    18-DEC-2000; 2000EP-0127688
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                                                                                                                                                 Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi H,
                               (first entry)
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PDSCEQQARNVQHYHK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 ptgtqdqarnaaqyhr 90
                                                                                                                 organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                         Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH67872
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                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa S,
Tateishi N,
                                 26-SEP-2001
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 AAG92653;
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AAB79449
ID AAB79
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AC AAB7
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DT 30-AB
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Gaps

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metabolism and oxidative phosphorylation (SMP) proteins given in metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors energy production. The C. glutamicum SMP gene can be used in vectors production of fine chemicals, such as, an organic acid, a proteinogenic or nomproteinogenic amino acid (preferred), a purine or pyrimidine base, or nomproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to
SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Corynebacterium glutamicum nucleic acid encoding a sugmetabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 737-738; 1246pp; English.
                                                                                                                                                                                                                                                                                                            99DE-1031424.
99DE-1031424.
99DE-1031428.
99DE-1031431.
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                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061975/07.
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                                                                                                                                                     MO200100844-A2
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09-JUL-1999;
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03-SEP-1999
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C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
                                                                                                                                                                                                                                                                                                                                                     SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleoside; lipid; saturated fatty acid; unsaturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum; carbon metabolism and energy production;
                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum SMP protein sequence SEQ ID NO:416.
                                                                                                         Score 43; DB 22; Length 388;
Pred. No. 69;
                                                                                                                                  7; Indels
                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                           AAB79450 standard; Protein; 388 AA.
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99DE-1031424.
99DE-1031428.
                                                                                                           36.4%;
                                                in a cell (i.e. ATP, NADPH).
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99DE-1042123
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                            30-APR-2001 (first entry)
                                                                                              Query Match
Best Local Similarity 43.00
                                                                                                                                                          3 PDSCEQQARNVQHYHK 18
                                                                                                                                                                                 79 ptgtqdqarnaaqyhr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99DE-1031
                                                                        388 AA;
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                                                                         Sequence
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                                                                       New isolated Corynebacterium glutamicum nucleic acid encoding a sugmetabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                  AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
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                               Schroeder H, Zelder O, Haberhauer G;
                                                                                                                                                                                                                                                                                                                   Score 43; DB 22; Length 388;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori cytoplasmic protein, 06ee10709orf5.
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                  Claim 20; Page 741-742; 1246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                AAW20743 standard; protein; 443 AA
                                                                                                                                                                                                                                                                                                                       36.48;
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95US-0487032
99DE-1042125
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                        3 PDSCEQQARNVQHYHK 18
                                                                                                                                                                                                                                                                                                                                                                         79 ptgtqdqarnaaqyhr 94
                                 'n
                                  Kroeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori.
                                                 WPI; 2001-061975/07
N-PSDB; AAF71567.
                                                                                                                                                                                                                                                                                                388 AA;
                  (BADI ) BASF AG.
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07-JUN-1995;
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03-SEP-1999;
                                  Pompejus M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW20743;
                                                                                                                                                                                                                                                                                                 Sequence
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(ASTR) ASTRA AB.

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Zea mays protein fragment SEQ ID NO: 50968.
                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                        AAG41011 standard; Protein; 74 AA.
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990S-0132484.
990S-0132485.
990S-0132486.
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99US-0123180.
99US-0123548.
99US-0125788.
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99US-0134218
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99US-0135353
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                                                                                                                    36.4%;
                                                                                                                                                                                                                                                                                                           18-OCT-2000 (first entry)
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165 ntpdskkissrnindhh 181
                                                                                                                                                                    1 NSPDSCEQQARNVQHYH 17
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays subsp. mays.
                                                                                                            Query Match
Best Local Similarity
7; Conserve
                                                                                   979 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1999;
06-APR-1999;
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21-MAY-1999;
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19-APR-1999;
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                                                                                     Sequence
                                                                                                                                                                                                                                      RESULT 29
                                                                                                                                                                                                                                                   AAG41011
                                                                                                                                                                                                                                                              The present sequence is a Helicobacter pylori cytoplasmic protein

Involved in cofactor metabolism.

The protein may be used in a vaccine to prevent or treat H. pylori

Infection or to identify H. pylori polypeptide binding compounds,

Useful as potential H. pylori life cycle activators or inhibitors.

Useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from

The genomic sequence of H. pylori antigent of the least 180 nucleotides,

Overlapping contigs generated by mechanically shearing the bacterial

Overlapping contigs generated by mechanically shearing the bacterial

Overlapping contigs generated by mechanically shearing the bacterial

Coverlapping contigs generated by mechanically shearing the bacterial

Coverlapping contigs generated by mechanically shearing the bacterial

Coverlapping contigs of the pylori antigens for vaccine development, the aminor defined sequences predicted from various ORF were analysed for significant and determined the sequences of interest, particular regions can be insolated from H. pylori by PCR amplification for recombinant polypeptide

Coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                             Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human CENP-C and its antibodies - for detecting anti-centromere antibodies in patients with auto-immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autoimmune rheumatic diseases; CREST syndrome; classification;
                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 18; Length 443;
Pred. No. 81;
6; Mismatches 4; Indels
                                                                                                                 Claim 61; Page 1158-1159; 1481pp; English.
         Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saitoh H, Tomkiel JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR34783 standard; Protein; 979 AA
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.4%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 scekiavnirhlyrsev 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SCEQQARNVQHYHKNEL 21
       Berglindh OT, Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; immunoassay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CENP-C antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-100976/12.
N-PSDB; AAQ38525.
                                  WPI; 1997-052306/05.
N-PSDB; AAT67996.
                                                                                                                                                                                                                                                                                                                                                443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Earnshaw WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9305151-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR34783;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
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protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                     ó
                               The sequence is that of the human CENP-C antigen which may be recombinantly produced in large amts. Thus the polypetide is available to more accurately classify patients with such autoimmune rheumatic diseases as CREST syndrome, and commercially useful quantities are available for use in diagnostic systems.
                                                                                                                                                                                                                                       Score 43; DB 14; Length 979;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                       5; Indels
Claim 17; Page 45; 68pp; English.
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US-0135629 US-0136392 US-0136392 US-013728 US-013728 US-013774 US-013804 US-0139143 US-0139143	990S-0139454. 990S-0139455. 990S-0139455. 990S-0139456. 990S-0139450. 990S-0139460. 990S-0139460. 990S-0139461. 990S-0139461. 990S-0139462. 990S-0139750. 990S-0139750. 990S-014063. 990S-014083.	20141384 1015-0141384 1015-014289 1015-014289 1015-014289 1015-014289 1015-014289 1015-014289 1015-014438 1015-014433 1015-014433 1015-014433 1015-014433	905 - 014481 905 - 014508 905 - 014508 905 - 014508 905 - 014508 905 - 014514 905 - 014514 905 - 014521 905 - 014591 905 - 014591 905 - 014591 905 - 014591 905 - 014591 905 - 014591
MAY 1999; -MAY 1999; -MAY 1999; -MAY 1999; -JUN 1999;	18 - 70N - 1999; 18 - 70N - 1999; 21 - 70N - 1999; 22 - 70N - 1999; 23 - 70N - 1999; 24 - 70N - 1999; 24 - 70N - 1999; 28 - 70N - 1999; 28 - 70N - 1999; 29 - 70N - 1999; 29 - 70N - 1999; 20 - 70N - 1999; 21 - 70N - 1999; 21 - 70N - 1999; 22 - 70N - 1999; 23 - 70N - 1999; 24 - 70N - 1999; 25 - 70N - 1999; 26 - 70N - 1999;	- Juli - 1999; - Juli - 1999;	1. JUL - 1999; 1. JUL - 1999; 1. JUL - 1999; 2. JUL - 1999; 2. JUL - 1999; 3. JUL - 1999; 3. JUL - 1999; 3. JUL - 1999; 7. JUL - 1999; 7. JUL - 1999; 7. JUL - 1999; 7. JUL - 1999; 8. JUL - 1999; 7. JUL
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990S-0146389 990S-01477038 990S-0147703 990S-0147302 990S-0147303 990S-0147416 990S-0147416 990S-0147416 990S-0147419 990S-0147935 990S-0148319 990S-0148341 990S-0148341 990S-014936 990S-014936 990S-0149723 990S-0149723 990S-0149723 990S-0149723 990S-0149930 990S-0149930 990S-0149930 990S-0149930	(0.5.0151489) (0.5.0151489) (0.5.0151930)	MUS-0115928/WS-0115928/WS-0115928/WS-0115928/WS-0115928/WS-0115938/WS-0115938/WS-0115938/WS-0115928/WS-0115928/WS-0115928/WS-0115928/WS-0116081198/WS-016081198/WS-016081198/WS-016081198/WS-016081198/WS-0161136
02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 10-AUG-1999; 113-AUG-19	- SEP - 1999 - SEP	2.0CT-1999 3.0CT-1999 3.0CT-1999 3.0CT-1999 4.0CT-1999 4.0CT-1999 4.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999 6.0CT-1999
7		7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

AAW20963 standard; Protein; 198 AA.

(first entry)

21-JUL-1997

AAW20963;

1 NSPDS-CEQOARNVQHYHKNE 20

|:|:| ||: 76 ntpnsgcekvdnlfkhyhnie

a

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This sequence is a H. pylori secreted or periplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial overlapping contigs generated by mechanically shearing the bacterial overlapping the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant hand determined the sequences of interest, particular regions can be included from H. pylori by PCR amplification for recombinant polypeptide isolated from H. pylori hosts.
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                                                                                                                                                                                                                                                                                                                                      Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.5; DB 18; Length 173; Pred. No. 48;
                                                      Length 74;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                             H. pylori secreted or periplasmic protein 663530.aa.
                                                         DB 21;
                                                                      Pred. No. 18;
0; Mismatches
                                                         Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 72; Page 715; 1481pp; English.
                                                                                                                                                                                                                          AAW20560 standard; Protein; 173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US09122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0630405.
95US-0487032.
99US-0161992.
99US-0161993.
99US-0162142.
                                                         35.2%;
66.7%;
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith D,
                                                                                                                     3 PDSCE-QQARNVQHY 16
                                                                                                                                                 pdrceaggarlegry 42
                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 AA;
                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT67707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1996;
07-JUN-1995;
 28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                     15-JUL-1997
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                                                                                                                                                                                                                                                        AAW20560;
                                                                                                                                                  28
                                                                                                                                                                                                              AAW20560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a H. pylori protein likely to be secreted or
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
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                                                              H. pylori secreted or periplasmic protein, hplp14013orf4.
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Pred. No. 56;
1; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 72; Page 1353; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                        96US-0630405.
95US-0487032.
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                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-052306/05.
N-PSDB; AAT68216.
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Matches 9; Conserv
                                                                                                                                                                                   Helicobacter pylori
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                                                                                                                                                                                                                                                                             06-JUN-1996;
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                                                                                                                                                        diagnosis.
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Gaps

Indels

7;

Mismatches

4

35.2%; nilarity 42.9%; Conservative 4

Query Match Best Local Similarity Matches 9; Conserv

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Gaps

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The peptide has an ability to promote formn. of B.subtilis extracellular protease. It is expressed in B.subtilis in high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA fragment encoding specific amino acid sequence · promotes formation of Bacillus subtilis extracellular protease.
                                                                                                                                                 SacUS2 confers DegU phenotype, and is encoded by part of the 2.55 kb Sall-Sphl SacU locus. This can restore levan saccharase synthesis in B. subtilis sacU- mutants, and overproduces proteins in this or other microorgansisms.
                                                   DNA contg. Bacillus subtilis sacU locus - for inducing overproduction in microogansisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide which promotes formn. of B. subtilis extracellular protease.
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Pred. No. 80;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%; Score 41; DB 10; Length 229; 50.0%; Pred. No. 80; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis; extracellular protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP91952 standard; peptide; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; page 439; 16pp; japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                    Claim 3; Fig 6; 87pp; French.
                                                                                                                                                                                                                                                                                                                 34.7%;
50.0%;
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Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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36 ddgdeaarivehyh 49
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36 ddgdeaarivehyh 49
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N-PSDB; AAN90668.
  WPI; 1989-309530/42.
N-PSDB; AAN91619.
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AAG82403
ID AAG824(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA fragment encoding specific amino acid sequence - has inhibitory activity for extracellular protease of Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptide has an inhibitory effect on the prodn. of extracellular protease in Bacillus subtilis. See also AAN90122.
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                                                                                                                                                                                                  peptide; inhibitor; Bacillus subtilis; extracellular protease.
                                                                                                                                   Polypeptide with inhibitory effect on prodn. of extracellular protease of Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 10; Length 139;
Pred. No. 45;
3; Mismatches 4; Indels
                    AAP90358 standard; protein; 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90995 standard; protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; page 14; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. subtilis sacUS2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 34.7%;
Best Local Similarity 50.0%;
Matches 7; Conservative 3
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36 ddgdeaarivehyh 49
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N-PSDB; AAN90122.
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                                                                                                                                                                                                                                       Sacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 39-NOV-1987;
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                                                             AAP90358;
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AAP90358
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Gaps

Cellulase; endoglucanase; cellobiohydrolase; celA.

Orpinomyces cellulase celA

Orpinomyces sp. strain PC-2.

WO9814597-A1

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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                 S. epidermidis open reading frame protein sequence SEQ ID NO:1900.
                                                 Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW56738 standard; Protein; 459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 34.7%;
70.0%;
                                                                                                                       09-NOV-2000; 2000WO-US30782
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                                                                          Staphylococcus epidermidis
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Best Local Similarity 70.v
Fra 7; Conservative
                     03-SEP-2001 (first entry)
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184 rdelhyhkne 193
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N-PSDB; AAH53253.
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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    AAG82403;
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AAW56738
ID AAW51
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DT 14-S
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) fand/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their reatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH5501 to sequences given in the sequence listing of the present specification, because the secuence is the present specification, however the sequence listing of the present specification, however the sequences are given in the disclosure for SEQ ID NO:4454 so even though sequences are present for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
Claim 18; Page 519; 2188pp; English.
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Gaps

This polypeptide comprises cellulase celA of Orpinomyces sp. strain OC-2, an anaerobic bovine rumen fungus Orpinomyces sp. PC-2. Its amino acid sequence was deduced from an isolated CDNA clone (see AAV5941). CelA has endoglucanase and cellobiohydrolase activity, with highest activity at pH 4.8 and 50 degC. CelB (see AAW56742) and celC (see AAW56739) cellulolytic enzymes of Orpinomyces sp. PC-2 are also proteins are claimed, as well as recombinant cells selected from Saccharomyces cerevisiae, Escherichia coli, Aspergillus, Trichoderma reesei, Pichia, Penicillium, Streptomyces or Bacillus, and a method for producing recombinant cellulase by

culturing these host cells.

Sequence

New recombinant DNA encoding Orphnomyces cellulase protein - useful for, e.g. producing recombinant Orpinomyces cellulase in host cell

Claim 1; Page 28-30; 69pp; English.

(UYGE-) UNIV GEORGIA RES FOUND INC.

96US-0027883.

97WO-US18008.

03-OCT-1997; 04-OCT-1996;

09-APR-1998

Chen H, Li X, Ljungdahl LG

WPI; 1998-240096/21. N-PSDB; AAV29471.

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protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
34.7%; Score 41; DB 19; Length 459; 42.9%; Pred. No. 1.8e+02;
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                                                                1 NSPDSCEQQARNVQHYHKNEL 21
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Best Local Similarity 42.9;
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Pred. No. 1.1e+02;
1; Mismatches 2; Indels
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25-FEB-2000; 2000EP-0301439.

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Pred. No. 2.2e+02;
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61 sskkckekfenvykyhk 77
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milarity 41.2%;
Conservative 3
990S-0159294.
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Matches 7; Conserv
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This sequence is a Drosophila melanogaster accessory gland protein (Acp) of the invention. A particular Acp, designated Acp62F, is toxic to insects, particularly to Drosophila and caterpillars, and it (or vectors that express it) can be used to kill or inhibit development of insect pests, for plant protection. More generally detection of Acp's in a female fruit fly is indicative of recent mating.
                                                                                                                                                                                                                                                                                                                                                                                                               Accessory gland protein; Acp; toxin; insecticide; Drosophila; mating; caterpillar; development inhibitor; insect pest; plant protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding accessory gland proteins of Drosophila
                                                                                                                                                                                                                  Length 597;
                                                                                                                                                                                                                 Score 41; DB 21; Length 59
Pred. No. 2.4e+02;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 38; Page 24-25; 89pp; English
                                                                                                                                                                                                                                                                                                                                 AAY22176 standard; Protein; 716 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tram K, Wolfner MF;
      990S-0160741.
99US-0160767.
99US-0160768.
99US-016078.
99US-0160814.
99US-0160980.
99US-0160980.
99US-0160989.
99US-0160989.
                                                                                                                                  99US-0161359.
99US-0161360.
99US-0161361.
                                                                                                                                                                                                                  34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0071315.
                                                                                                                                                                 39US-0161920
                                                                                                                                                                                              99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila Acp36DE protein.
                                                                                                                                                                                                                                                                             108 sskkckekfenvykyhk 124
                                                                                                                                                                                                                                                           SPDSCEQQARNVQHYHK 18
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                          Ouery Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-418871/35.
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                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9932149-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
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                                                                                                                                                                                              29-0CT-1999
                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                    AAY22176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lung O,
                             -0cr-1
                                                                                                                                                                 18-0CT-1
                                                                                                                                                                          8-0CT-1
                                                                                                              -001-
                                                             oc<u>r</u>
                                                                     50-150
                                                  21-OCT-
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716 AA;

Sequence

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Gaps

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ANY54086-99 represent enzymes involved in the biosynthesis of
exopolysaccharides (EPS). These enzymes are designated EPSA-EPSN, and
are encoded by open reading frames epsA-epsN. The enzymes are isolated
from Lactobacillus delbrueckii bulgaricus. The proteins are used
in a method for the synthesis of EPS, which includes at least one step
of forming a bond (alpha or beta-isomer) between C-1 (carrying the
ce of forming allehyde function, of an activated D-galactose pyranose), and
ce phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis
of EPS occurs with in each step, addition of a new sugar unit, through
its heari-acetyl function, to an alcoholic hydroxyl of a second sugar
out, present at the end of a chain of sugar residues bonded to the
primer. EPSA is attenuator of transcription which influences
ce primer. EPSA is attenuator of transcription which influences
involved in the control of the molecular weight and/or the length of the
polysaccharide; EPSD, EPSL and EPSM are involved in synthesis of EPS;
EPSE is a glactosy- or glucosyl-phospho-transferase which catalyses the
transfer of the first saccharide on the primer; EPSF and EPSG are
calpha-glycosyltransferases; EPSG is a glucosyltransferase; EPSK is
                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exopolysaccharide; EPS; ESP enzyme; EPSB; EPSB; EPSB; EPSB; EPSF; EPSF; EPSG; 
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of
                                                               4
Length 716;
                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzyme EPSJ involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cheese; flavour stability; organoleptic property.
   DB 20;
3e+02;
   Score 41; DB 2
Pred. No. 3e+02
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 18; Page 156-157; 162pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus delbrueckii bulgaricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamothe G;
                                                                                                                                                                                                                                                                                                                                           AAY54095 standard; Protein; 327 AA
                                                                                                                                                             || ||| :|: |: |303 spgqleqqillhlqnllhfqqnql 326
                                                                                                                           2 SPDSCEQQ----ARNVQHYHKNEL 21
                                                                  5;
   Query Match 34.7%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98EP-0201310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NEST ) SOC PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fermented milk products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-097267/08.
N-PSDB; AAZ45260.
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22-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1999
                                                                                                                                                                                                                                                                                                                  AAY54095
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acidified milk products (yoghurt or cheese).

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Gaps

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ANY 43788-89, AAY 43791-Y437801 and AAY 43842 represent the enzymes encoded by the eps operon of Lactobacillus delbrueckii bulgaricus Lfi5. The operon contains 14 open reading frames, and encodes enzymes (epsh, epsC, epsD, epsE, epsE, epsC, epsB, epsC, epsE, epsC, epsC,
responsible for the polymerisation of the repetitive units; and EPSN is responsible for export of the EPS. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or problotic properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eps operon; Lactobacillus delbrueckii bulgaricus Lfi5; enzyme; epsA; epsB; epsC; epsE; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-013255/01.
N-PSDB; AA230357, AAY43796, AAY43797, AAX43798, AAY43799, AAY43800,
AAY43801, AAY43842.
                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of epsJ of L. delbrueckii bulgaricus Lfi5.
                                                                                                                                                                                                                           Length 327;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                           Score 40.5; DB 21;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 18; Page 157-158; 163pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus delbrueckii bulgaricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stingele F, Germond JE, Lamothe G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY43797 standard; Protein; 327 AA
                                                                                                                                                                                                                                                                                                                                      2 SPDSC-----EQQARNVQHYHK 18
                                                                                                                                                                                                                                                                                                                                                                         40 spdscpkicdeysqkfnnvkvvhk 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                           Query Match
34.3%;
Best Local Similarity 41.7%;
Matches 10; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP03011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09954475-A2
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22-APR-1998;
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                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY43797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
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              888888
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cequences AAB38321-B38396 represent the amino acid sequences of 62
human secreted proteins encoded by the genes AAC69512-C69587. The genes
and proteins are useful for preventing, ameliorating or treating medical
conditions, e.g. by protein or gene therapy. The genes are isolated from
a range of human tissues disclosed in the specification. The nucleic
acids, proteins, antibodies and (antipagonists are useful in the
cidsnosis, treatment and prevention of: (a) autoimmune diseases e.g.
chagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
of the breast or liver; (c) cardiovascular disorders e.g. cardiac
arrest; (d) carebrovascular disorders e.g. cardiac
infections caused by bacteria, viruses and fung; and (h) ocular
disorders e.g. corneal infection. The polypeptides can also be used to
disorders e.g. corneal infection. The polypeptides can also be used to
ading due to sunburn, to maintain organs before transplantation, for
supporting cell culture of primary tissues, to regenerate tissues and in
                                                                                                   .,
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives .
                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shi Y;
Birse CE;
                                                                                                                                                                                                                                                                                                                                            fragment of human secreted protein encoded by gene 10 clone HTEBV72.
                                                                   Length 327;
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Moore PA,
                                                                                                   Indels
                                                     Score 40.5; DB 21.
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Florence KA,
                                                                                  Pred. No. 1.56
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 32; 716pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i J, Komatsoulis GA,
Olsen HS, Ebner R,
                                                                                                                                                                                                                                                    AAB38431 standard; peptide; 40 AA.
                                                                                                                                      2 SPDSC-----EQQARNVQHYHK 18
                                                                                                                                                                   63
                                                                                                                                                           40 spdscpkicdeysqkfnnvkvvhk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                        34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1999; 99US-0128693.
26-APR-1999; 99US-0130991..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000; 2000WO-US08979.
                                                                                                                                                                                                                                                                                                                    31-JAN-2001 (first entry)
                                                                           Query Match
Best Local Similarity 41.7
Matches 10; Conservative
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                            Ä
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                            327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Ni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lafleur DW
Young PE;
                                                                                                                                                                                                                                                                                       AAB38431;
                              Sequence
                                                                                                                                                                                                                       43
                                                                                                                                                                                                                       RESULT 4
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40

Sequence

31.2%;

Best Local Similarity

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Gaps

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buman secreted proteins encoded by the genes AAC69512-C69587. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the acids, proteins, antibodies and (ant)agonists are useful in the chematoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to all wound healing and epithelial cell proliferation; to prevent skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                             cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmalogical; human; vulnerary; gene therapy; infection; secreted protein.
                                                                                                                                                                                                                                                                                             Fragment of human secreted protein encoded by gene 10 clone HTEBV72.
                                                                                                                                                                                                                                                                                                                             antiarthritic; antirheumatic; antiproliferative;
   21; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soppet DR,
, Moore PA,
                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, S
Florence KA,
 Score 40; DB:
Pred. No. 16;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 32; 716pp; English.
                                                                                                                                                                                      AAB38428 standard; peptide; 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Komatsoulis GA, Olsen HS, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
33.9%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0128693.
990S-0130991.
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                                                                                                                                                                                                                                                           (first entry)
                                 Conservative
                                                                                                   24 tpevieksvrdlehwh 39
                                                                   SPDSCEQQARNVQHYH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lafleur DW, Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-647418/62.
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                 Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200061623-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young PE;
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ID AAB3
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            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant organ morphogenesis control and determn. - by regulating the expression of homeotic genes which determine the identity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 231;
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            Indels
                                                                                                                                                                                                                   Plant; organ morphogenesis; control; petunia; petals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 14; LA
Pred. No. 1.2e+02;
7; Mismatches 7;
             4;
                                                                                                                                                                                                                                                                                                                                                                                                   Van DER KROL AR;
Pred. No. 83;
                                                                                                                                                                                            Product of homeotic gene "green petal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG59547 standard; Protein; 246 AA.
                                                                                                                     AAR43385 standard; Protein; 231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 74pp; English.
            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                    Kush A,
                                                                                                                                                                                                                                                                                                                                        92US-0867580
92US-0909589
                                                                                                                                                                                                                                                                                                                 93WO-US03508
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nqietfkkkvrnveeihrnll
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                                                                                                                                                                     (first entry)
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Best Local Similarity 33.3
Matches 7; Conservative
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117 tpevieksvrdlehwh 132
               Conservative
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See also AAR43386-7
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06-JUL-1992;
                                                                                                                                                                     19-JUN-1994
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               2;
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Shi Y; Birse CE;

DB 21; Length 171;

Score 40;

33.98;

Query Match

171 AA;

Sequence

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990S-0148311.
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09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
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27-AUG-1999;
    23 - JUN - 1999
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01 - JUL - 1999
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05-AUG-1999;
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19-JUL-1999;
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19-JUL-1999;
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 77032.
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990S-0134376.
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99US-0132407
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990S-0126785
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99US-0128234
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                                         Arabidopsis thaliana
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990S-0139454.
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01-APR-1999;
06-APR-1999;
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21-APR-1999;
23-APR-1999;
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41.2%;
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99US-0159638.
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102 dvlghkarnyhhlhqnq 118
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Best Local Similarity 41.2
Matches 7; Conservative
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28-OCT-1999;
29-OCT-1999;
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26-OCT-1999;
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PR 01-701-1999 9908-0141842.

PR 06-701-1999 9908-0142056.

PR 06-701-1999 9908-0142050.

PR 13-701-1999 9908-0142372.

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PR 13-701-1999 9908-014332.

PR 19-701-1999 9908-014408.

PR 19-701-1999 9908-0144332.

PR 20-701-1999 9908-0144333.

PR 20-701-1999 9908-0147346.

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PR 20-701-1999 9908-0144333.

PR 20-701-1999 9908-014333.

PR 20-701-1999 9908-014333.
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protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 1.3e+02;
3; Mismatches 7; Indels
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106 dvlghkarnyhhlhqnq 122
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Best Local Similarity 41.2

Best Local Similarity 41.2

Conservative
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Pred. No. 1.3e+02;
3; Mismatches 7;
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99US-0123180.
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990S-0159584.
990S-0160741.
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99US-0159331.
99US-0158369.
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106 dvlghkarnyhhlhqnq 122
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Best Local Similarity
Matches 7; Conserva
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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24-SEP-1999;
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01-SEP-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 1.4e+02;
2; Mismatches 7; Indels
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99US-0123180.
99US-0125788.
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99US-0127462.
99US-0128234.
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99US-0129845.
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PR 05-ANY-1999; 99US-013248.
PR 06-ANY-1999; 99US-013248.
PR 06-ANY-1999; 99US-013248.
PR 11-ANY-1999; 99US-013248.
PR 11-ANY-1999; 99US-013248.
PR 14-ANY-1999; 99US-013428.
PR 16-ANY-1999; 99US-013523.
PR 25-ANY-1999; 99US-013523.
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PR 27-JUN-1999; 99US-013943.
PR 27-JUN-1999; 99US-013943.
PR 17-JUN-1999; 99US-014332.
PR 17-JUN-1999; 99US-014332.
PR 17-JUN-1999; 99US-014333.
PR 17-JUN-1999; 99US-014433.
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Query Match
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 7; Indels

Search completed: December 17, 2001, 07:50:51 Job time: 73 sec

us-09-462-625-1.oli.rng

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Murine granulocyte
Primer EBI8203 for
Primer EBI8203 for
Human secreted pro
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DNA encoding prote Human tag7 clone c Human Htag7 secret Chondrosarcoma pep

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                              the tag7 DNA sequence are used to express recombinant tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypebtide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as prihars. Antibodies against tag7 are used as reagents for detecting tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                        sequence encodes the murine tag? of the invention. Cells containing
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; Pred. No. 5.9e-269;
0; Mismatches 0;
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This cDNA sequence encodes the precursor (see AAW23723) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAW23725). It was isolated from murine bone marrow CDNA using primers based on bovine BGP-A cDNA (see AAW3725). It was comprises signal peptide and propeptide sequences followed by 12 c-terminal amino acids corresponding to mature MGP-A mid amino acids corresponding to mature MGP-A and Gram-negative bacteria, fungi and viruses, specifically Staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolyaccharides, e.g. sepsis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtgcccgcagtgagtggaggcctgccatccgagtgctctagccgcctggggcaccca 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atgitigititgcctgtgctctccttgccctcgggtctggcaacctcctgcagtttcatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels : 0;
Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis; endotoxaemia; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%; Score 379; DB 18; Length 677; 100.0%; Pred. No. 1.2e-182; ive 0; Mismatches 0; Indels '(
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36..581
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/product= MGP-A
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Best Local Similarity 100.
Matches 379; Conservative
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This sequence is a PCR primer for DNA encoding the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; so as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour metastasis.
                                                           carcinoma; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
gaacagcaggcccgcaatgtgcagcattaccacaagaatgagctgggctggtgcgatgta
                              216 gaacagcaggcccgcaatgtgcagcattaccacaagaatgagctggggctggtgcgatgta
                                                                                                                                                                                                                                                                                                                                                                                                                                    melanoma; leukaemia; apoptosis inducer; mouse; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokhorchouk E;
                                                                                                                                                                                                                                                                                                                                                                                         Primer EB18203 for Mouse tag7 clone coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        growth inhibitor; mammalian tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41 BP; 6 A; 13 C; 11 G; 11 T; 0 other;
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                                                                                                                                                                                                    396 aacttcatggaccgggtac 414
                                                                                                                                                                                     361 aacttcatggaccgggtac 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-120887/10
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Length 41;

DB 20; 0.21;

Score 22; Pred. No.

4.0%; 5

Query Match Best Local Similarity

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This sequence is a PCR primer for DNA encoding the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tunmours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, panceas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma, sarcoma (Raposi's, osteo- or fibro-sarcomas), polypeptide inhibits tumour growth and induces apoptosis. The tag7 coling sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour metastasis.
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 Gaps
                                                                                                                                                                                                                                                                Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; mouse; PCR primer; ss.
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100.0%; Pred. No. 0.21;
Live 0; Mismatches 0; Indels
   Indels
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   0; Mismatches
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                                 528 ctgggaacactaccgagagtga 549
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                                                   41 CTGGGAACACTACCGAGAGTGA 20
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                                                                                                                                         AAX21834 standard; DNA; 41
                                                                                                                                                                                                        (first entry)
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    Conservative
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nes 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seorgiev G,
                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1999
                                                                                                                                                                                                        18-MAY-1999
    22;
                                                                                                                                                                                                                                                                                                                  Synthetic.
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Matches
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AAA80662
ID AAA80
      Matches
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(first entry)

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arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraphoteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of
                                                                                                                         Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; nephritis; hyperproliferative disorder; cardlovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious diseases. The human secreted protein gene #8 and protein sequences are represented in sequences AAA80613 and AAB25583. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAB0606-AB06023 encode the 12 secreted protein sequences given in AAB05576-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant. antilammatory; antiarthritic; antirheumatic, dermatological; antiproliferative, antiarthritic; antirheumatic, dermatological; antiproliferative, antiarthritics antirheumatic, wilnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rhemmatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA80662-A80663 represent genes related to the secreted protein gene#8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases
                                                                                 Human secreted protein gene #8 related gene HBMTB79R SEQ ID #115.
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                                                                                                                                                                                                                                                                                      melanoma; lymphoma; wound healing; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Olsen HS, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 757; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                          21-NOV-2000
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AAA80662;
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Wei Y;

Kenny JJ, Moore PA,

99WO-US25031. 98US-0105971.

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The present invention describes an antibody that binds to a human protein (I) selected from: PRO181; PRO1269; PRO1410; PRO1755; PRO1780; PRO344; PRO1927; PRO1567; PRO1295; PRO12039; PRO14034; PRO1934; PRO1934; PRO1935; PRO18035; PRO18034; PRO1934; PRO1905; PRO1906; PRO1908; and PRO2626. (I) has anticancer activity and cam be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferrably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AACS8019 to AACS8012 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AACS8103 to AACS8122 and AAB24021 to AAB24040 represent human sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression -
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                                                                                                                                proliferation; cancer;
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                                                                                                                                        Human; tumour; diagnosis; neoplastic disease; proliteratio
identification; tumourigenesis; anticancer; detection; ss.
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                                                                                                   Human PR01269 nucleotide sequence SEQ ID NO:6.
                                                                                                                                 diagnosis; neoplastic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.0%; Score 22; DB 100.0%; Pred. No. 0.1 ative 0; Mismatches
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            BP.
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99WS-0162506.
99WO-US28313.
99WO-US28634.
            AAC58104 standard; cDNA; 697
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                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                          08-MAR-1999;
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                                             AAC58104;
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AAC58104
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Gaps

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0; Indels

4.0%; Score 22; DB 21; Length 285;

ed. No. 0.19; Mismatches

Pred. No.

100.0%; Pr tive 0;

Conservative

Query Match Best Local Similarity Matches 22; Conserval

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Goddard A, Gurney AL,
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980S-0106248
980S-0106384
980S-0106464
980S-0106856
980S-0106905
980S-0106905
980S-0106919
980S-0106919
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9803-0106023.
9803-0106029.
9803-0106030.
9803-0106032.
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98US-0108787.
98US-0108788.
98US-0108801.
                   98US-0102487.
98US-0102570.
98US-0102570.
98US-0102681.
98US-0102687.
98US-0103268.
98US-0103368.
98US-0103318.
98US-0103318.
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98US-0103318.
98US-0103318.
98US-0103318.
98US-0103318.
98US-0103318.
98US-0103401.
98US-0103673.
98US-0103673.
98US-0104577.
98US-0104577.
98US-0104577.
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98US-0105881.
98US-0105882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker K,
                                                 Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
                                    Human PRO1269 (UNQ639) cDNA sequence SEQ ID NO:215.
                                                                                                                                       98US-0098716.
98US-0098749.
98US-00988750.
98US-0098803.
98US-00998736.
98US-0099536.
98US-0099598.
98US-0099598.
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98US-0100388.
98US-0100390.
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98US-0099763.
98US-0099792.
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98US-0100627.
98US-0100661.
98US-0100664.
98US-0100684.
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                                                                                                                            99WO-US20111
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98US-010127
                     08-AUG-2000 (first entry)
                                                                                             WO200012708-A2
                                                                                Homo sapiens.
                                                                                                                           01-SEP-1999;
                                                                                                            09-MAR-2000
       AAA37082;
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Wood WI;

Watanabe CK,

Smith V,

or

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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO
                                   New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                              Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;
                                                                                                                                                                                                                        polypeptides from the present invention.
                                                                                        Claim 2; Fig 121; 773pp; English
                                                                                                                                                                                                                                                                                                                                                                   525 tcaaaggacaccgggatgtgca 546
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF54356 standard; DNA; 697
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                                                                                                                                                                                                                                                                                                                  Conservative
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WPI; 2000-237871/20;
P-PSDB; AAY99400.
                                                                                                                                                                                                                                                                                                  Local Similarity
hes 22; Conserv
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                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia
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                                     AAX21820
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                           Gaps
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4.0%; Score 22; DB 21; Length 697;
100.0%; Pred. No. 0.19;
                          0; Indels
                           Mismatches
                                                                                                                                                                                                                   DNA encoding protein of the invention #61.
                                                                                                                                                                                                                                           Secreted; transmembrane; gene therapy; ss.
 4.00,
100.08; Pre-
                                                   tcaaaggacaccgggatgtgca 482
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99WO-US30095
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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene

WPI; 2001-071395/08

Fong S; Hillan KJ;

Ferrara N,

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This sequence encodes the human tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leuksemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptiosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antagonist tag7; for isolating tag7 and therapeutically to inhibit or delay tumour metastasis.
                                                                                                                                                                                                                                                                                          ö
                                                    The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                        Gaps
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melanoma; leukaemia; apoptosis inducer; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding tag? - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
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                                                                                                                                                                                                                                                         Score 22; DB 22; Length 697; Pred. No. 0.19;
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                                                                                                                                                                                                  Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX21820 standard; cDNAto mRNA; 718 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tag7 clone coding sequence.
                            Claim 2; Fig 121; 787pp; English.
                                                                                                                                                                                                                                                                                                                                461 tcaaaggacaccgggatgtgca 482
                                                                                                                                                                                                                                                                                                                                                                     525 tcaaaggacaccgggatgtgca 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-EP04287.
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Best Local Similarity 100.v
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P-PSDB; AAY00771.
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which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; (Zrohn's disease; nephititis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAB0006-AB0063 encode the 12 secreted protein sequences given in AAB25576-625593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; antiarmatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of the beautiful antibacterial and antideced and antagonists may be used to treat prevent and/or diagnose various disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                                                Gaps
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                                                                         DB 20; Length 718; 0.19;
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                Sequence 718 BP; 142 A; 251 C; 194 G; 131 T; 0 other;
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                                                                         4.0%; Score 22; DB illarity 100.0%; Pred. No. 0.1 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                            Human Htag7 secreted protein gene #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Figure 34; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wounds, and infectious diseases
                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                     · 461 tcaaaggacaccgggatgtgca 482
                                                                                                                                                                          552 tcaaaggacaccgggatgtgca 573
                                                                                                                                                                                                                                                                                           AAA80613 standard; cDNA; 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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                                                                                            Local Similarity
nes 22; Conserv
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                                                                           Query Match
                                                                                                                                                                                                                                                      RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; regulator; chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #8 and protein sequences are represented in sequences AAA80613 and AAB2583. Sequences AAA80662-A80663 represent genes related to the secreted protein gene#8.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Chondrosarcoma peptidoglycan recognition protein-like protein cDNA.
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                                                                                                                                     DB 21; Length 726; 0.19;
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                                                                                           Sequence 726 BP; 161 A; 251 C; 188 G; 126 T; 0 other;
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55..645
/*tag= a
/*product= PGRP-like_protein
55..117
                                                                                                                                                                   0; Mismatches
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                                                                                                                                       Score 22;
Pred. No.
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                                                                                                                                       4.0%;
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118..642
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Best Local Similarity 100.
Matches 22; Conservative
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P-PSDB; AAY96964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
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10 gagtggagggcctgccatcc 30

73 gagtggagggccctgccatcc

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63

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This sequence is a PCR primer for DNA encoding the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express the recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas) melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis; The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antagonist of tag7; for isolating tag7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
                                                                                                                                                                               Gaps
associated with tumour necrosis factor (TNF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; melanoma; leukaemia; apoptosis inducer; mouse; PCR primer; s
                                                                                                                                        4.0%; Score 22; DB 21; Length 749; 100.0%; Pred. No. 0.19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutically to inhibit or delay tumour metastasis
                                                                                       Sequence 749 BP; 165 A; 259 C; 195 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer EB18471 for Mouse tag7 clone coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Page 75; 138pp; English.
                                                                                                                                                                                                                                       461 tcaaaggacaccgggatgtgca 482
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                                                                                                                                                                                                                                                                                                                                            AAX21828 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1999 (first entry)
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georgiev G, Kiselev S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-120887/10.
                                                                                                                                              Query Match
Best Local Similarity
Matches 22; Conserv
                                                         pulmonary fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9902686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia
                                                                                                                                                                                                                                                                                                                                                                                  AAX21828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
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the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13633 to AAH13641 represent human cDNA sequences; AAB92446 to AAH93633 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence complementary to a polynucleotide comprises a 1'-end sequence complementary to a polynucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDMAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
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Otsuki'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3580 BP; 917 A; 909 C; 949 G; 805 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 18086; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sogai T, Nishikawa T, Hayashi K, S.
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                   Human cDNA sequence SEQ ID NO:18086.
            AAH18181 standard; cDNA; 3580 BP
                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                 EP1074617-A2.
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
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                                                          AAH18181;
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AAH18181
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DB 22; Length 3580;

3.5%; Score 19;

Query Match

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Query Match
3.8%; Score 21; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels

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463 aaaggacaccgggatgtg 480

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression -
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                        Gaps
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                        Indels
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Pred. No. 5.9;
Mismatches
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99WO-US20111.
99US-0162506.
99WO-US28313.
  Best Local Similarity 100.0%;
Matches 19; Conservative (
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                                                                    25 gccctcctgggtctggcaa 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594320/56.
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29-OCT-1999;
30-NOV-1999;
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ID AAC5
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                                                                                                                                                                                                                                                                                                                                                                                                Fong S;
Hillan KJ;
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Gurney AL, 1
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The nucleic acids may also be used in gene therapy
                                                                                        Primer #130 used in the identification of proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Pred. No. 23;
Mismatches 0;
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Pred. No.
                                                                                                                  Secreted; transmembrane; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 143; Page 507; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Botstein D, Desnoyer
oddard A, Godowski PJ,
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                     BP
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99WO-US30095.
2000WO-US00219.
2000WO-US00376.
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99US-0144758.
99US-0145698.
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99WO-US28313
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Pan J, Paoni NF, Roy MA,
Watanabe CK, Williams PM,
                                                                                                                                                                                                                18-FEB-2000; 2000WO-US04342
                                                                                                                                                                                                                                                                              99WO-US20111
                   AAF54520 standard; DNA; 18
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                                                                    02-APR-2001 (first entry)
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nes 18; Conserv
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06-JAN-2000;
                                                                                                                                           Unidentified
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26-JUL-1999;
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                                             AAF54520;
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Matches
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Search completed: December 17, 2001, 10:30:37

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Gaps

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3.3%; Score 18; DB 21; Length 18; 100.0%; Pred. No. 23; ive 0; Mismatches 0; Indels

Query Match 3.3 Best Local Similarity 100. Matches 18; Conservative

Job time: 5051 sec

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1 ATGTTGTTTGCCTGTGCTCTCCTTGCCTCCTGGGTCTGGCAACCTCCTG
/SIDS8/gcgdata/geneseg/genesegn/NA1997.DAT:AAT78850
/SIDS8/gcgdata/genesegn/RA1995.DAT:AA081489
/SIDS8/gcgdata/genesegn/Genesegn/NA1997.DAT:AAT93872
/SIDS8/gcgdata/geneseg/genesegn/NA2000.DAT:AAT60186/gcgdata/genesegn/Genesegn/NA2001.DAT:AAD60186/gcgdata/geneseg/genesegn/NA2001.DAT:AAD609976
                                                                                                                                                                                                                                                                                                                                                                          Mouse tag7 clone coding sequence.
                                                                                                                                                                                                 seq_documentation_block:
ID AAX21819 standard; cDNA; 549 BP.
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Ratio: 5.473
Percent Similarity: 100.000
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US-09-462-625-2 x AAX21819
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P-PSDB; AAY00770.
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342
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-Q-Cgn2_1/USPTO_spool/USO9465625/runat_17122001_074948_26126/app_query.fasta_1.241
-DB-N_Geneseq_1101 -DOMT-fastap -SUFFIX-p2n.rng -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-GAPOP-4.500 -GGAPEXT-0.050 -XGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YAPACP-10.000 -YGAPEXT-0.500
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_CORRE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFWT-pfs
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4.4e-08
6.1e-08
0.0008
0.0003
0.4457
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221.78
225.08
164.34
135.60
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1920.84
1401.67
1401.67
1401.34
1401.34
1400.87
1368.94
808.63
808.63
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343.07
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                                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        -NORM-ext -MINLEN=0 -MAXLEN-2000000000
-USER-US09462625_@CGN1_1_272 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secore Lines:
Strd Orig Zscore Escore Len 1D
Sequence
SIDSB/gcdata/geneseq/geneseqn/NA1999. DAT.AAX21819 + 9
SIDSB/gcgdata/geneseq/geneseqn/NA1000. DAT.AAA37082 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA37082 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA37082 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA37082 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA31820 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA31820 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA31091 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA80613 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA31719 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA31719 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA21719 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA21719 + 6
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA21311 + 3
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA21311 + 3
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA15311 + 3
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA1531 + 3
SIDSB/gcgdata/geneseq/geneseqn/NA2000. DAT.AAA1331 +
          OM of: US-09-462-625-2 to: N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
Query: US-09-462-625-2
Query length: 182
Database: N_Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (Sec): 166.110000
                                                          Date: Dec 17, 2001 11:25 AM
                                                                                                                                                                               Command line parameters:
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the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours sepecially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Raposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as probes for gene mapping are used as reagents for detecting tag7; sa an antagonist tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the murine tag? of the invention. Cells containing
   36.92
58.13
58.13
58.13
74.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
129.90
126.36
126.36
126.36
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   84.00
84.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ostermann E, Prokhorchouk E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 549 BP; 117 A; 161 C; 151 G; 120 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 182
Gaps: 0
Percent Identity: 100.000
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Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis; endotoxaemia; mouse; ss.
                                                                                                                                                                                                                          rPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLeuArgA 134
                                                                                                                                                                                                                                                          AsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProGl·167
GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa 67
                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT78510
                                                                                                                                                                                                                                                                  (pos:561..563, aa:Trp)
                                                                                              67 IGINHİSTYRHİSLYSASNGLULEUGLYTTPCYSASPVALALATYRASNP
                                                                                                      yAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                  Murine granulocyte peptide A precursor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
36..581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/transl_except=
543..578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product- MGP-A
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This cDNA sequence encodes the precursor (see AAM23723) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAM23725). It was isolated from murine bone marrow cDNA using primers based on bovine BGP-A cDNA (see AAT78509). The encoded MGP-A precursor comprises signal peptide and propeptide sequences followed by 12 comprises signal peptide and propeptide sequences followed by 12 creminegative bacteria, fungitatively against Gram-positive and BGP-A (see AAW23724), exhibit activity against Gram-positive and cram-negative bacteria, fungi and viruses, specifically can be Staphylococcus aureus, Bscherichia coli, Candida albicans, Salmonella typhimurium and c. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat claimed) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce supplies (claimed). They can also be applied to crops to reduce the supplies claimed). They can also be applied to crops to increase
                                                                                                                                    Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heLeulleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGlyAspHisThrGlyProIleTrpAsnProMetSerIleGlyIleTh 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        They have low immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sSerPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erSerArgLeuGlyHisProValArgTyrValValIleSerHisThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 677 BP; 146 A; 217 C; 171 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 1
Percent Identity: 97.253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                            Claim 14; Fig 5; 56pp; English.
96US-0011834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                their disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAT78510
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5.336
97.253
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US-09-462-625-2 x AAT78510
                                (REGC ) UNIV CALIFORNIA
                                                                                                WPI; 1997-424753/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                 P-PSDB; AAW23723
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16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                 Selsted ME;
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500

250

84

200

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The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1401; PRO1755; PRO1780; PRO1434; PRO1927; PRO1567; PRO1269; PRO1403; PRO4344; PRO1567; PRO1269; PRO1269; PRO1364; PRO4364; PRO4364; PRO4367; PRO4367; PRO16056; PRO20626. (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonaclectide which preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present human PRO sequences. AAC58103 to AAC58102 and AAB24021 to AAB24040 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
identification; tumourigenesis; anticancer; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe CK,
                                                            150
                                                                                         482
                                                                                                                                                         532
                              432
                                                                                                                         167
134
                                                                                                                                                                                                                                                      seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC58104
                                                            rPhemetGlyAsnPhemetAspArgValProAlaLysArgAlaLeuArgA
                386 CTTCATGGGGAACTTCATGGACCGGGTA...CGCAAAGCGGCCCTCCGTG
                                                                                                                                                         ASDTYIGLUVALLYSG1yHisArgAspValGlnSerThrLeuSerProG1
                                                                                                                                                                                                         yAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1269 nucleotide sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 50; Fig 3; 226pp; English
                                                                                                                                                                                                                                                                                                     BP
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99WO-US28313.
99WO-US28634.
                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAC58104 standard; cDNA; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US05028
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; AAB24022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
30-NOV-1999;
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01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1999
                                                                                                                                                                                                                                                                                                                                      AAC58104;
                                                                                                                         151
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117
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PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 ValSerArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAs 159
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                                                                                                                                                                                                                                                                                          rCysGluGlnGlnAlaArgAsnValGlnHisTyrHisLysAsnGluLeuG
                                                                                                                                                                                                                                                                                                                                                                           76 lyTrpCysAspValAlaTyrAsnPheLeuIleGlyGluAspGlyHisVal
                                                                                                                                                                                                                                                                                                                                                                                     91 GGAGACAGAAGACCCGGCCTGCTGCAGCCCCATAGTGCCCCGGAACGAGT
                                                                                                                                                                                                                                                                                                                                               1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer..
                                                                                                                                                                                                                                                    26 rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
                                 Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;
                                                                         189
                                                                                           Percent Identity: 67.196
                                                                         Length:
                                                                                                                                                 :
20
                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAA37082 standard; cDNA; 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
                                                                         692.00
4.325
84.656
                                                                                                                                                Align seg 1/1 to: AAC58104
                                                                                                                  alignment_block:
US-09-462-625-2 x AAC58104
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                                                                          Quality:
Ratio:
Percent Similarity:
                                                                   alignment_scores
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New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or
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98US-0106905
98US-0106905
98US-0106919
98US-0106919
98US-0106934
98US-01069775
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980S-0103315.
980S-0103325.
98US-0102571.
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98US-0102687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker K, Goddard A,
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P-PSDB; AAY99400.
                                                                                                     08-0CT-1998;
08-0CT-1998;
14-0CT-1998;
20-0CT-1998;
20-0CT-1998;
22-0CT-1998;
22-0CT-1998;
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06-0CT-1998;
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07-0CT-1998;
07-0CT-1998;
07-0CT-1998;
08-0CT-1998;
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   Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
    Human PRO1269 (UNQ639) cDNA sequence SEQ ID NO:215.
                                                                                                                                                                                                                                                                                                                                                                                           980S-0101471.
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980S-0101474.
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98US-0099536.
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23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
                                                 Homo sapiens.
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29-SEP-1998;
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                                                                                           01-SEP-1999;
                                                                                                                                                                  09-SEP-1998;
                                                                             09-MAR-2000.
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Wood WI;

Watanabe CK,

Smith V,

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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 GGAGACAGAAGACCCGGCCTGCTGCAGCCCCATAGTGCCCCGGAACGAGT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer.. 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ATGCTGCTTGCCTGGGCTCTCCCCAGCCTCCACTCGGAGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 TyrvalvalileSerHisThrAlaGlySerPheCysAsnSerProAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 697 BP; 136 A; 250 C; 184 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 67.196
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                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAA37082 from: 1 to: 697
                                  claim 2; Fig 121; 773pp; English
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84.656
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591 ATTGGCCACACTACCGC 607

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seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF54356
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DNA encoding protein of the invention #61
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99US-0162506.
99WO-US28313.
99WO-US28551.
99WO-US30095.
2000WO-US00219.
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99US-0144758.
99US-0145698.
                                                                                          2000WO-US04342
     697
                          (first entry)
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ID AAF54356 standard;
                                                                    WO200078961-A1.
                                                                                          18-FEB-2000;
                                                                                                                                                      06-JAN-2000;
                          02-APR-2001
                                                          Unidentified
                                                                                                                                                 05-JAN-2000;
                                                                                                                                           16-DEC-1999;
                                                                               28-DEC-2000
                                                                                                                26-JUL-1999
                                                                                                                      01-SEP-1999
                                                                                                                           29-0CT-1999
                                                                                                                                30-NOV-1999
                                                                                                                                      02-DEC-1999;
                AAF54356;
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(GETH) GENENTECH INC.

Fong S; Hillan KJ; Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D; Watanabe CK, Williams PM, Wood WI;

WPI; 2001-071395/08

Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene therapy

Claim 2; Fig 121; 787pp; English

The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.

BP; 136 A; 250 C; 184 G; 127 T; 0 other; Sequence 697

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189
1
67.196
                           Percent Identity:
       Length:
                  Gaps:
                   4.32584.656
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                                                  alignment_block:
US-09-462-625-2 x AAF54356
         Quality:
                           Percent Similarity:
alignment_scores
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from: 1 to: 697 Align seg 1/1 to: AAF54356 1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer.. 16 us-09-462-625-2.p2n.rng

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Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma;
melanoma; leukaemia; apoptosis inducer; human; ss.
                                                                                                                                                                                                                    pasnprometSerIleGlyIleThrPheMetGlyAsnPheMetAspArgV 126
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                                                                                                                                                                                                                                                                                                             pvalGlnSerThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnS
                                                                                                         Prokhorchouk E;
                                                                                                                                                                                          191 TATGIGGIGGIATCGCACACGCCGCGCGCACCTGCAACACCCCCCGCCTC
                                                                                                                                              lyTrpCysAspValAlaTyrAsnPheLeuIleGlyGluAspGlyHisVal
                                                                                                                                                       43 TyrvalvalileSerHisThrAlaGlySerPheCysAsnSerProAspSe
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26 rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
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_AAX21820 standard; cDNAto mRNA; 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tag7 clone coding sequence.
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the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Raposi's, stomach, pancreas, mouth, head somethy marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 polypeptide inhibits tumour growth and induces apoptosis and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7, for isolating tag7 and therapeutically to inhibit or delay tumour tag7.
                                               New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uaps: 1
Percent Identity: 67.196
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                                                                                                                                                                                                                 Claim 11; Page 126-127; 138pp; English
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4.325
84.656
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WPI; 1999-120887/10.
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                                     P-PSDB; AAY00771
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          NAME OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS OF COLORS O
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AAA80606-B2593. The human secreted proteins have various activities of the proteins include: immunosuppressant; activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; anticonner; vulnerary; antiarthritic; anticonner; vulnerary; antiproliferative; and antifungal activity. The proteins, polypeptides, agonists and antifungal activity. The proteins, polypeptides, agonists and antifungal activity the proteins, and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephitis; cardiovascular disorders e.g. coronary arteriosciarosis and mycoarditis; cardiovascular disorders e.g. coronary arteriosciarosis and mycoarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antichematic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; cronn's disease; inchnitis; hyperproliferative disorder; cardiovascular disorder; coronry arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autolumune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases
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                    567
                                                       pvalGlnSerThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnS 176
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                                                                                                                                                                                                                     seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA80613
568 IGIGERACACTCTCTCAGGCAACCAGCTCTACCACCTCATCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                 Human Htag7 secreted protein gene #8.
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                                                                                                                                                                                                                                                                             AAA80613 standard; cDNA; 726
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                                                                                                                                                             176 erTrpGluHisTyrArg 181
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P-PSDB; AAB25583.
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                                                                                                                                                                                                                                                                                                                    AAA80613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ni J,
                    518
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sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #8 and protein sequences are represented in sequences AAA80613 and AAB25583. Sequences AAA80662-A80663 represent genes related to the secreted protein gene#8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 TACGAGGGCCGTGGCTGGAACTTCACGGGTGCCCACTCAGGTCACTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrvalvallleSerHisThrAlaGlySerPheCysAsnSerProAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 rCysGluGlnGlnAlaArgAsnValGlnHisTyrHisLysAsnGluLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 ValSerArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAs
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                                                                                                                                                                                                                                                                               1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer..
                                                                                                                                                                                                                                                                                                  26 rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
                                                                             Sequence 726 BP; 161 A; 251 C; 188 G; 126 T; 0 other
                                                                                                                                                        Gaps: 1
Percent Identity: 67.196
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ID AAA51719 standard; cDNA; 749
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4.325
84.656
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31-OCT-2000

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Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; bovine granulocyte peptide A; BGP-A; preservative; sepsis; endotoxaemia; cattle; ss.
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                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                          126 alproalaLysArgAlaLeuArgAlaAlaLeuAsnLeuLeuGluCysGly 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 ValSerArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAs 159
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120 GGAGACAGAAGACCCGGCCTGCTGCAGCCCCATAGTGCCCCGGAACGAGT 169
                                                                                                                                                                                                                                    76 lyTrpCysAspValAlaTyrAsnPheLeulleGlyGluAspGlyHisVal 92
                                   42
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                                                                                                   109 pasnProMetSerIleGlyIleThrPheMetGlyAsnPheMetAspArgV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 TyrGluGlyArgGlyTrpAsnileLysGlyAspHisThrGlyProlleTr
                                                       rpArgAlaLeuProSerGluCysSerSerArgLeuGlyH1sProValArg
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29.601
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29.91
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ID AAT78509 standard; cDNA; 688
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/product= E
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                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcomatissue (PGRP-K) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antison presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumnour necrosis factor (TMF) and TNF-like cytokines, auch as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic pulmonary fibrosis.
                                                                            Peptidoglycan recognition protein-like protein; PGRP-C; regulator; chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
                                              Chondrosarcoma peptidoglycan recognition protein-like protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer.. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....CysSerPhelleValProArgSerGluT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 67.196
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55..645
/*tag= a
/product= PGRP-like_protein
55..117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 3; 191pp; English
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118..642
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                     (first entry)
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84.656
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US-09-462-625-2 x AAA51719
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3-DEC-1998; 22-DEC-1999;

06-JUL-2000

mat_peptide

sig_peptide

Ношо

alignment_scores:

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152
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                                                                                                                                                                                                                                                                                                                                                             treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity.
                                                                                                                                                                                                                                                             This cDNA sequence encodes the precursor (see AAW23722) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated bovine granulocyte peptide A or BGP-A (see AAW23724). It was isolated from bovine pentide A or BGP-A (see AAW23724). It was procedures. The encoded BGP-A precursor comprises a 21-amino acid signal peptide, a 156-residue propertide and 13 C-terminal amino acids corresponding to mature BGP-A. BGP-A and the murine homologue, MGP-A (see AAW23725), exhibit activity against Gram-positive and Gram-negative bacteria, fundi and viruses, specifically Staphylococcus aureus, Escherichia coli, candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to
                                                                                                                                                                     Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AGAGGCTAAGACAGCCTGTGCGCTACGTGGTGTGTCGCACACGGCGGGC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 GlyAspHisThrGlyProlleTrpAsnProMetSerIleGlyIleThrPh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eulleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIleLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 rPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysSerS 35
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Percent Identity: 68.333
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                             96US-0011834
 97WO-US02218
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4.418
85.000
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                                                                                                                          WPI; 1997-424753/39.
P-PSDB; AAW23722.
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Ratio:
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13-FEB-1997;
                             16-FEB-1996;
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Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; yulnonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer;
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/product= "Human full length zgpal protein #2 with
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                                                                                                                                                                                                                                                       TyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProGlyAs 168
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                      402
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD04006
                                                                                                                                                                                                                                                                                       118 eMetGlyAsnPheMetAspArgValProAlaLysArgAlaLeuArgAlaA
                                                                                                135 laLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSerAsn
                                                                                                                                                                                                                                                                                                                                                        pGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArg 181
                                                                                                                                                                                                                                                                                                                                                                                                     553 CGAGCTCTATAAAATCATCCAGCAGTGGCCGCACTACCGC 592
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12-JUL-2000; 2000US-0218070.
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/*tag= b
52..1107
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ID AAD04006 standard;
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peptide (GP-A) homolog, Zgpal protein. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, canti-microbial activity are useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, urinary tract for infections, respiratory infections, vaginal infections, acquired immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infection in skin and other epithelial wounds. Spal-cytokine fusion proteins are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion covarians infections such as bacterial, viral or fungal infection and incroorganism infections such as bacterial, viral or fungal infection and antibodies, polynucleotides and polypeptides are useful for antibodies, polynucleotides and polypeptides are useful sequences are useful for cancering genetic diseases or cancers. Zgpal sequences are useful for 5 non-coding regions of a zgpal gene. Zgpal sequences are useful for 5 non-coding regions of a zgpal gene. Zgpal antibodies are useful for 5 squal genetal express zgpal, for screening expression libraries and cancerizing antibodies or as antagonists to block zgpal antibodies or as antagonists to block zgpal antibodies or as antagonists to block zgpal antibodies or as antagonists to conserve zgpal interaction of tagging cells that express zgpal, in a setving as antagonist to block zgpal antibodies or as antagonists to conserve zgpal interaction in cell cultury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1110 BP; 249 A; 319 C; 295 G; 247 T; 0 other;
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in vitro and in vivo. Zgpal gene is also useful
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The present sequence is a cDNA encoding human full length granulocyte peptide (GP-A) homolog, Zgpal protein. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies within are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, uninary tract infections, respiratory infections, vaginal infections, acquired immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infection in skin and other epithelial wounds. Expal-cytckine fusion proteins are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion proteins are useful in in vitro studies of exogenous
                                                                                                                                                                                                                                                                                                         Humān; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory;
vulnerary; dermatological; anti-microbial; gastrointestinal disease;
pulmonary; dental carries; periodontal disease; gene therapy; AIDS;
Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis;
infection; urinary tract; respiratory; vaginal; lung; skin; cancer;
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/product= "Human full length zgpal protein #1 with
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seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD04004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       ovarian; rectal; chromosome 1; ss.
                                                                                                                                                           seq_documentation_block:
ID AAD04004 standard; cDNA; 1128 BP
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12-JUL-2000; 2000US-0218070.
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P-PSDB; AAE00692.
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(first entry)

31-OCT-2000

AAA51718;

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microorganism infections such as bacterial, viral or fungal infection and also to study epithelial cell defensin induction in cell culture. Zapal antibodies, polynuclectides and polypeptides are useful for detection of zapal polypeptide, mRNA or anti-zapal antibodies, thus serving as markers for detecting genetic diseases or cancers. Zapal sequences are useful as diagnostics in forensic DNA profiling and as probes or primers to clone 5' non-coding regions of a zapal gene. Zapal antibodies are useful for tagging cells that express zapal, for screening expression libraries and as neutralizing antibodies or as antagonists to block zapal activity in vitro and in vivo. Zapal gene is also useful in gene therapy.
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                                                                                                                                                                                                                                                                      Sequence 1128 BP; 255 A; 321 C; 300 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 Length: 169
Gaps: 2
Percent Identity: 43.787
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US-09-462-625-2 x AAD04004
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                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                Ratio
                                                                                                                                                                                                                                                                                                                                                     alignment_scores
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            8888888888888
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seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA51718

seq_documentation_block: ID AAA51718 standard; cDNA; 1876

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expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in sugmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TNF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
                                             Wound healing tissue peptidoglycan recognition protein-like protein cDNA.
                                                                            Peptidoglycan recognition protein-like protein; PGRP; PGRP-W; regulator; wound healing tissue; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          saps: 3
Percent Identity: 44.910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen HS;
                                                                                                                                                                                       Location/Qualifiers
107..1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2A-B; 191pp; English.
                                                                                                                                                                                                                    /*tag= a
/product= PGRP-W
107..157
/*tag= b
158..1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                       99WO-US30736.
                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0113809.
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3.279
71.856
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US-09-462-625-2 x AAA51718
                                                                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452414/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                              WO200039327-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1998;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1999;
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                                                                                                                                                                                                                                                    sig_peptide
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                                                                                                                                                                                                                                                                                  mat_peptide
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us-09-462-625-2.p2n.rng

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43
Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 5' EST: expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTACCTTCATGGGCACCTTCACAGGTATACCACCCAATGCTGCAGCAC 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1109 ACTCCCAACTACCTGCTGGGCCACAGTGATGTGGCCCGAACCTTGTC 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 euArgAlaAlaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 ArgSerAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSe 165
                                                                                                                                                                                                                                                                                                                                                                                       AsnileLysGlyAspHisThrGlyProIleTrpAsnProMetSerIleGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ylleThrPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaL 132
                                                                                                                                                                                                                                                                         811
                                                                                                                                                                          861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 rProGlyAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArg 181
                                                                                                                                                                                                                                                                                                                                                     86
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      48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 5' EST isolated from a cDNA library SEQ ID NO:308
                                                   762 GACCACTGTCCAGGATGACTCTCCCAGCGAAGTATGGCATCATTATCCAC
      32 uCysSer.SerArgLeuGlyHisProValArgTyrValValIleSerHis
                                                                                                                       49 ThralaGlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaAr
                                                                                                                                                                          312 ACTGCCGGGAGGACCTGCAACATTTCTGATGAGTGCCGCCTGCTGGTCCG
                                                                                                                                                                                                                                     65 gAsnValGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaT
                                                                                                                                                                                                                                                                                                                                                  yrAsnPheLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrp
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AC
AA242549;
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AA242549;
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O1-FEB-2000 (first entry)
XX
Human 5' EST isolated from a cDD
XX
W gene therapy: chromosome mapping
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Homo saplens:
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AAX4200 TO AAX4307 TEPICESENT HOVEL 3 explesses sequences, corresponding to human secreted proteins. AAX6451 to AXX65438 represent the EST-related proteins corresponding to AAX42265 to AXX65438 represent the EST-related proteins corresponding to AAX42265 to AXX43052. The 5' ESTS can be used for producing secreted human gene corresponds. The ESTS can identify and isolate 5' untranslated corresponds upstream regulatory regions which control the regions (UTRS) and upstream regulatory regions which control the credion, development stage, rate, and quantity of protein synthesis, as concluding a stability of maNA. The ESTS are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTS can also be used in forensic procedures to identify individuals, or in calcable from abnormal gene expression. The products may also be used in forensic procedures conditionally and importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane, or importing a polypeptide into a membrane and membrane and the identification of new secreted proteins is therapeutic value, and the identification of new secreted proteins is sequences used in the exemplification of the present invention.
                                                 AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 rCysGluGlnGlnAlaArgAsnValGlnHisTyrHisLysAsnGluLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 lyTrpCysAspValAlaTyrAsnPheLeu.IleGlyGluAspGlyHisVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 .....CysSerPheileValProArgSerGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 GGAGACAGAAGCCGGCCTGCTGCTGCATAGTGCCCCGGAACGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 380 BP; 67 A; 130 C; 114 G; 63 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  percent Identity: 62.162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
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Claim 1; Page 336; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: AAZ42549 from: 1
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ID AAD04007 standard; cDNA; 1107 BF
XX
AC AAD04007;
XX
DT 02-JUL-2001 (first entry)
XX
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3.989
78.378
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Ratio:
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uCysSerSerArgLeuGlyHisProValArgTyrValValIleSerHisT

513 GCNTGYCCNGGNGTNGTNCCNMGNWSNGTNTGGGGNGCNMGNGARACNCA

CNGCNGGNMGNACNTGYAAYATHWSNGAYGARTGYMGNYTNYTNGTNMGN 759

hrAlaGlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArg

49 710 :::::||| :::::|| GAYATHCARWSNTTYTAYATHGAYMGNYTNAARWSNTGYGAYATHGGNTA rAsnPheLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpA

091 82

66 ASNVALGINHISTYTHISLYSASNGluLeuGlyTrpCySASpValAlaTy

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Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystlc fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer;
                                                                                                                                                                                                                                                                            New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
Human full length Zgpal cDNA #2 degenerate sequence.
                                                                                                                                                                                                                                                                                                                         Claim 3; Page 111; 114pp; English.
                                                                         ovarian; rectal; chromosome 1; ss
                                                                                                                                                                                20-OCT-1999; 99US-0160712.
12-JUL-2000; 2000US-0218070.
                                                                                                                                                            20-OCT-2000; 2000WO-US29177
                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                       Conklin DC, Adler DA,
                                                                                                                                                                                                                                                         WPI; 2001-290918/30
                                                                                                                    WO200129224-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy
                                                                                                 Homo sapiens
                                                                                                                                        26-APR-2001
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Fox BA;

snileLysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGly 115

860 AYGINCARGGNWSNWSNACN...CCNGGNTAYGAYGAYATHGCNYINGGN 116 IleThrPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLe

859

66

149 rgSerAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSer 165

1007 CNCCNAATTAYYTNYTNGTNGGNCAYWSNGAYGTNGCNMGNACNYTNWSN

166 ProGlyAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArg

```
This sequence is stated as encoding human truncated granulocyte peptide (GP-A) homolog, Zgpal protein. This sequence is a degenerate version of the coding region of SEQ ID NO: 7 shown in AAD04006. Zgpal gene is concated on human chromosome 1. Zgpal polypeptides are useful for located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating chartal carries, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, respiratory infections, vaginal infections, caquired immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infections in skin and other chancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are useful in in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal culture. Zgpal antibodies, polynucleotides and polypeptides are useful colluce. Zgpal antibodies, polynucleotides and polypeptides are useful scatection of zgpal polypeptide, mRNA or anti-zgpal antibodies, thus carefulng as markers for detecting genetic diseases or cancers. Zgpal colone 5' non-coding regions of a zgpal antibodies, caprossion libraries and as neutralizing antibodies or as antagonists to block the colone 5' non-coding regions of a zgpal gene is also useful in hower than an activity in vitro and in vivo. Zgpal gene is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1107 BP; 186 A; 117 C; 201 G; 144 T; 459 other;
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Human, granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer;
1057 CCNGGNCARGCNYTHTAYAAYATHATHWSNACNTGGCCNCAYTTYAAR 1104
                                    seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AADO4005
                                                                                                                                                             Human full length Zgpal cDNA #1 degenerate sequence.
                                                                                                                                                                                                                                                               ovarian; rectal; chromosome 1; ss
                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOX BA;
                                                                  seq_documentation_block:
ID AAD04005 standard; cDNA; 1125
                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1999; 99US-0160712.
12-JUL-2000; 2000US-0218070.
                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000WO-US29177
                                                                                                                                        02-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adler DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-290918/30
                                                                                                                                                                                                                                                                                                                       WO200129224-A2
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conklin DC,
                                                                                                                                                                                                                                                                                                                                                  26-APR-2001
                                                                                                               AAD04005;
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16 SerCysSerPhelleValProArgSerGluTrpArgAlaLeuProSerGl 32

to: 1107

Align seg 1/1 to: AAD04007 from: 1

alignment_block: US-09-462-625-2 x AAD04007

Percent Identity: 36.747

344.00 3.215 64.458

Ratio:

Quality:

alignment_scores

Percent Similarity:

Length: Gaps:

New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections

Claim 3; Page 106-107; 114pp; English.

caquired immune deficiency syndrome (AIDS) and lung infections associated attented immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infection in skin and other with cystic fibrosis and prevention of infection in skin and other central properties are useful for more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, more specifically lung, ovarian and rectal cancers). Zgpal polypeptides of fragments, fusion proteins or agonists are useful in in vitro studies of infection and also to study epithelial cell defensin induction in cell infection and also to study epithelial cell defensin induction in cell culture. Zgpal antibodies, polynucleotides and polypeptide, mRNA or anti-zgpal antibodies, thus sevenences are useful as diagnostics in forensic DNA profiling and as probes or primers to clone 5' non-coding regions of a zgpal gene. Zgpal ontibodies are useful for tagging cells that express zgpal, for screening expression libraries and as neutralizing antibodies or as antagonists to block zgpal activity in vitro and in vivo. Zgpal gene is also useful in (GP-A) homolog, Zgpal protein. This sequence is a degenerate version of the coding region of SEQ ID NO: 4 shown in AAD04004. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, respiratory infections, vaginal infections, sequence is stated as encoding human truncated granulocyte peptide

Sequence 1125 BP; 191 A; 117 C; 204 G; 146 T; 467 other;

82 rAsnPheLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpA 99 66 AsnValGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTy 82 16 SerCysSerPhelleValProArgSerGluTrpArgAlaLeuProSerGl 32 32 uCysSerSerArgLeuGlyHisProValArgTyrValValIleSerHisT 49 49 hralaglySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArg 65 Gaps: 2 Percent Identity: 36.747 Length: to: 1125 to: AAD04005 from: 1 344.00 3.215 64.458 alignment_block: US-09-462-625-2 x AAD04005 Quality:
Ratio:
Percent Similarity: alignment_scores: Align seg 1/1

snileLysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGly 115

66 378

116 IleThrPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLe 132 AYGTNCARGGNWSNWSNACN...CCNGGNTAYGAYGAYGAYTHGCNYTNGGN 924

ATHACNITYATGGGNACNITYACNGGNATHCCNCCNAAYGCNGCNGCNYT 974

925

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BG187105 RST6088 Athersys RA
BG46743 EST36 Pacific oyste
A1849253 UT-M-AJI-agz-e-10-0
A930493 vo45c06.rl Barstead
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metacoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 589)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissuc_type="lumor, blopsy sample"
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Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
174 c 161 g 128 t
                                                                                                                                                                                                  EST 06-FEB-2001
musculus cDNA clone IMAGE:4457680 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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Gaps: 0
Percent Identity: 100.000
       4.8e-27
1.6e-26
3.8e-26
1.3e-25
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/organism="Mus musculus"
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                                                                                                                                                                                                       BG174272 589 bp mRNA 602334571F1 NCI_CGAP_Mam1 Mus
       650.09
640.68
633.89
624.18
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       352.00
349.00
342.00
336.50
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Ratio: 5.473
Percent Similarity: 100.000
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US-09-462-625-2 x BG174272
                                                                                                                                 seq_name: gb_est2:BG174272
                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                  BG17427
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gb_est1:AI849253
gb_est1:AA930493
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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AW076051 xa83g01.x1 NCI_CGAP_CM
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                                                                                                                    software, version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    out_format : pfs
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.4e-42
.6e-42
                                                                                                                 About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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996.00 1847.37
996.00 1847.37
996.00 1846.58
991.00 1837.84
983.00 1837.84
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                                                                   Date: Dec 17, 2001 10:56 AM
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us-09-462-625-2.p2n.rst

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samples: Gilbert Smith, NIH"
167 g 137 t
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AK008335.1 GI:12842459
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a 196 c
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Ratio: 5.473
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KEYWORDS
SOURCE
                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bamalla; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. It (bases 1 to 637)

NIH-MCO http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

Contact: Robert Strausberg, Preparation: LiA.G.E. Consortium (LLNL)

Found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
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602848402F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5011897
                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 lahlaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                       117 rPheMetGlyAsnPheMetAspArgValProAlaLySArgAlaLeuArgA 134
                                                                                                                                                                                                                                                                                                                                            406
                                                                                                                                                                                                                                   101 LysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGly11eTh 117
                                       67 IGINHISTYTHISLYSASNGluLeuGlyTrpCysAspValAlaTyrAsnP
                    {\tt GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa}
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block: 682 bp mRNA HTC 05-JUL-2001 LOCUS AK008335 682 bp small intestine CDNA, RIKEN full-length DEFINITION Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAP trapper. Mus musculus (strain:C57BL/6J) adult male small intestine cDNA Mus musculus (strain:C57BL/6J) editions clone_lib:RIKEN full-length enriched mouse cDNA library clone:2010107E11.
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                                                                                                                                                                                                                51 GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa
Length: 182
Gaps: 0
Percent Identity: 100.000
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BG244455 688 bp mRNA EST 13-FEB-2001 602356590F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4485071 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                              Percent Identity: 100.000
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                                                                                     /note="putative"
682
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217 c 175
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BG244455.1 GI:12754270
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Ratio: 5.473
Percent Similarity: 100.000
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                                                                                                                            polyA_site
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Direct Submission
Submitted (10-JUJ-2000) Yoshihide Hayashizaki, The Institute of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                     Shibate, K. Ttoh, M. Aizawa, K., Nagaoka, S.; Sasaki, N., Carninci, P., Shibate, K., Ttoh, M., Aizawa, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwadi, K., Fujiwake, S., Inoue, K., Togawa, W., Isawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN Integrated sequence analysis (RISA) system-1384-format Sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="small intestine" /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                             genes
       Muridae; Murinae; Mus
                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Titoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome_research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
(pases 1 to 682)
     Mammalia; Eutheria; Rodentia; Sciurognathi;
                            1 (bases 1 to 682)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musnamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnamalia; Eutheria; Prodentia; Sciurognathi; Muridae; Musnamalia; It of 550)

Si MIH-MGG http://mgc.nci.nih.gov/
Bational Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Onpublished (1999)

Gontact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.
Colla Library Preparation: Life Technologies, Inc.
Colla Library Preparation: Life Technologies, Inc.
Colla Library Preparation: Life Technologies, Inc.
Colla Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:
Colla Library Arrayed by: Collone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1094 row: Collumn: 12
High quality sequence stop: 637.
                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block: 650 bp mRNA EST 05-JUL-2001
LOCUS B1155774 650 bp mRNA DEFINITION 602904343F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033867
                                                                                                                                                                                                     Length: 182
Gaps: 0
Percent Identity: 99.451
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Ratio: 5.445
Percent Similarity: 100.000
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US-09-462-625-2 x BI155774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: mammary; vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 1209 c 180 g 142 t
                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Contact: Role Strausberg, Contact: Robert Strausberg, Contact Strausberg, Inc.
Cond Library Preparation: Life Technologies, Inc.
Cond Library Preparation: Life Technologies, Inc.
Cond Library Preparation: Liprage Genomics, Inc.
Cond distribution: MGC clone distribution information can be found through the I.M. M.G.E. Consortium/LINL at:
http://image.lld.gov
plate: LiAMN0326 row: C column: 24
High quality sequence stop: 587.
High quality sequence stop: 587.
                                                                         Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Rodentla; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 688)

1 (bases 1 to 688)

Nath-MGC http://mag.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Percent Identity: 100.000
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/organism="Mus_musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
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Ratio: 5.473
Percent Similarity: 100.000
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US-09-462-625-2 x BG244455
                                                         house mouse
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lyaspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
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99.454
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US-09-462-625-2 x BI154844
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                    FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 610)
Sulf-McC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS B1154844 610 bp mRNA EST 05-JUL-2001
DEFINITION 602902826F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5032278 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 ATGTTGTTTGCCTGTGCTCTCCTTGCCTCGGGTCTGGCAACCTCCTG 120
                                                                                                                                     121 CAGTTTCATCGTGCCCCCCCAGTGAGTGGAGGCCCTGCCATCCGAGTGCT 170
                                                                                                                                                                                                                                 220
                                                                                                                                                                                                                                                                                                            270
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                                                                                                                                                                                                                                                                                                                                                                        heLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIle 100
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                                                                                                                                                                                                                1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSerCy
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                                                                                                                                                                                                                                                                      51 GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa
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  to: 650
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BI154844
BI154844.1 GI:14614845
to: BI155774
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Align seg 1/1
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VERSION
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/note="Organ: mammary; Vector: pcMv-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: Lihis is a NCL_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 PheLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 ITCCTTATTGGAGGAGGACGGTCATGTCTATGAAGGCCGAGGCTGGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 610
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     0
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         column:
                           610.
Plate: LLAMilus
High quality sequence stop: v
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

ACCESSION

sed_name:

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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: McC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnh.gov
Plate: LLAM9203 row: b column: 05
High quality sequence stop: 622.
High quality sequence stop: 622.
I. 706
Cocation/Qualifiers
I. 706
Corganism="Mus musculus"
Corganism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF163190 706 bp mRNA EST 30-OCT-2000 601771917F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3990820 5',
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233 c 187 g 146 t
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11 (bases 1 to 706)
12 (bases 1 to 706)
13 (bases 1 to 706)
14 (bases 1 to 706)
15 (bases 1 to 706)
16 (bases 1 to 706)
17 (bases 1 to 706)
18 (bases 1 to 706)
18 (bases 1 to 706)
18 (bases 1 to 706)
18 (bases 1 to 706)
18 (bases 1 to 706)
18 (bases 1 to 706)
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                                                                                                                                                                                                                                                                                                                                                                                       151 ASNTYLGLUVALLYSGLYHISATGASPVALGLNSETTHLLEUSETPLOGI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGlyIleTh 117
                                                                                                                                                                                                        167 yAspGlnLeuTyrGlnValIleGlnSer.TrpGluHisTyrArgGlu 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est2:BF163190
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LOCUS BF163190
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dr. Average insert size 1.3 kb. Constructed by Life
dr. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                   BG871384 600 bp mRNA EST 29-MAY-2001
602790566F1 NCI_CGAP_SG2 Mus musculus CDNA clone IMAGE:4921697 5',
                                                                                                                                                                                                                                                                                                                                                                                                                        L (Dases 1 to 000)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAM10840 row: d column: 18

High quality sequence stop: 585.
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 GGCAGCTTCTGCAACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 erSerArgLeuGlyHisProValArgTyrValValIleSerHisThrAla 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSerCy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 ATGTTGTTTGCCTGTGCTCTCCTTGCCCTCCTGGGTCTGGCAACCTCCTG
          531 GTGACCAACTCTATCAGGTCATCCAAAGCTGGGAACACTACCGAGAG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 98.907
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5.385
99.454
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US-09-462-625-2 x BG871384
                                                                                                                                                                                                  mRNA sequence.
BG871384
                                                               gb_est2:BG871384
                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                   seq_documentation_block:
LOCUS BG871384
                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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source

FEATURES

alignment_scores

BASE COUNT ORIGIN

34

51

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Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                     176 g
                                                                                                                                                                                                                                                                                                                                                                                                           Library."
202 c
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5.372
98.361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-462-625-2 x BG975104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG975104 645 bp mRNA EST 12-JUN-2001
602843369F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979057 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. H (bases 1 to 645).
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 laalaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 rPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLeuArgA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 GCAGCATTACCACAAGAATGAGCTGGGCTGGTGGAGTGTAGCCTACAACT 311
                                                                                                                                                                                                                                                                                                                    211
                                                                                                                                                                                                                                                                                                                                                                                261
                                                                                                                                                                                        62 AIGTIGITIGCCIGIGCICTICCTIGCCCTCGGGTCTGGCAACCTCCTG 111
                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                       GlySerPheCysAsnSerProAspSerCysGluGlnAlaArgAsnVa
                                                                                                                                                                                                                                                                                                                                                                    67 lGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnP
                        Length: 182
Gaps: 0
Percent Identity: 99.451
                                                                                                                                to: 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG975104.1 GI:14362741
                                                                                                                                 Align seg 1/1 to: BF163190
                                        Ratio: 5.324
Percent Similarity: 100.000
                         969.00
                                                                                    alignment_block:
US-09-462-625-2 x BF163190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:BG975104
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BG975104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS BG975104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                           Quality:
              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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ACCESSION VERSION

AUTHORS TITLE JOURNAL COMMENT REFERENCE

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/clote corganization 7, 3-11 (1996). Note: this is a NCI_CGAP
                                                                    рę
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10976 row: j column: 18
High quality sequence start: 3
High quality sequence stop: 634.
High quality sequence stop: 634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGlyIleTh 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 sSerPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysS 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 CAGTTTCATCGTGCCCCGCAGTGAGTGGAGGCCCTGCCATCCGAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 97.814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 645
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us-09-462-625-2.p2n.rst

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BI409815
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="texo":10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BE913706 1045 bp mRNA EST 29-SEP-2000
DEFINITION 601669059F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3969014 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9146 row: e column: 15
High quality sequence stop: 618.
High quality sequence stop: 618.
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MIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 sSerPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysS 34
                                        151 ASnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProGl 167
                                                                                                                                                                                                                                                                                                    caps: 2
Percent Identity: 98.370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE913706.1 GI:10411594
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98.913
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US-09-462-625-2 x BE913706
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BE913706
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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can be
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LOCUS B1409815 842 bp mRNA musculus cDNA clone IMAGE:5117688 5',
DEFINITION 602961906F1 NCI_CGAP_LU33 Mus musculus cDNA clone IMAGE:5117688 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus subraryos; Chordata; Craniata; Vertebrata; Euteleostomi; Butaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 842)
1 (bases 1 to 842)
NH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1991)
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Contect: Robert Strausberg, Ph.D.
Email: grapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Generaling by: Incyte Genomics, distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 GlyAspGlnLeuTyrGlnVallleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa
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EST 21-NOV-2000 musculus cDNA clone IMAGE:4166360 5'

BF302505 619 bp mRNA 602031534F1 NCI_CGAP_SG2 Mus mRNA sequence.

BF302505
BF302505.1 GI:11249045

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seq_documentation_block:
                                     DEFINITION
                                                                ACCESSION
                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                        COMMENT
        153 AACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGTGCAGCATTACCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euLeuGluCysGlyValSerArgGlyPheLeuArgSerAsnTyrGluVal 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 ITCTGGAATGTGGGGTGTCTCGGGGCTTCCTGAGATCCAACTATGAAGTC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 luAspGlyHisValTyrGluGlyArgGlyTrpAsnIleLysGlyAspHis 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 ThrGlyProlleTrpAsnProMetSerIleGlyIleThrPheMetGlyAs 121
                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 GCCACCCAGTTCGCTACGTGTCTCACACACACCCGGCAGCTTCTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                               21 lProArgSerGluTrpArgAlaLeuProSerGluCysSerSerArgLeuG 38
                                                                                                                                                                                                                                                                                                                                                             5 CysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSerCysSerPheIleVa
                                                                                                                                                                                                                                                                                                                                                                           3 TGTGCTCTCCTCGCCCTTATGGGTCTGGCAACCTCCTGCAGTTTCATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                           38 lyHisProValArgTyrValValIleSerHisThrAlaGlySerPheCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 sLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnPheLeuIleGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 AGGACGGTCATGTCTATGAAGGCCGAGGCTGGAACATCAAGGGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AsnSerProAspSerCysGluGlnGlnAlaArgAsnValGlnHisTyrHi
                                                                                                                                                                                                                                                                    Percent Identity: 98.315
                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                    to: 842
/clone="IMAGE:5117688"
                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                           965.00
5.483
98.876
                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BI409815
                                                                                                                                                                                                                                                                                              alignment_block:
US-09-462-625-2 x BI409815
                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                              201
                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                              BASE COUNT
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Not!; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                             Manualitation, Determine to the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of the season of th
                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 TGGGGCACCCAGTTCGCTACGTGTGATCTCACACACAGCCGGCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 CysAsnSerProAspSerCysGluGlnGlnAlaArgAsnValGlnHisTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 rHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnPheLeuIleG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 99.441
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    619
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: BF302505
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Ratio: 5.330
Percent Similarity: 100.000
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house mouse.
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ORIGIN
                             ORGANISM
                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
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us-09-462-625-2.p2n.rst

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Gaps:
Percent Identity:
                                                                                                                                                        Length:
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                                                                 б
                                                               187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA238752
AA238752.1 GI:1862775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 rTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                     US-09-462-625-2 x BE199698/rev
                                                               159 c
                                                Barstead.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGAACACTACCGAGAG
                                                                                                                                                                           5.441
98.266
                                                                                                                                                        925.00
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                                                                                                                                                              Quality:
                                                                                                                                                                                             Percent Similarity:
                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                     alignment_block:
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DEFINITION
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VERSION
KEYWORDS
SOURCE
                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M.; Hillier, L.; Kucaba, T.; Martin, J.; Beck, C.; Wylie, T.;
Underwood, K.; Steptce, M.; Theising, B.; Allen, M.; Bowers, Y.; Person, B.; Swaller, T.; Gibbons, M.; Pape, D.; Harvey, N.; Schurk, R.; Ritter, E.; Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.; Waterstron, R. and Wilson, R.

The WashU-NI Mouse EST Project 1999
Unpublished (1999)
Cother ESTs: ug52cil.yi
Cother ESTs: ug52cil.yi
Cother ESTs: ug52cil.yi
Cother ESTs: ug52cil.yi
Cother ESTs: ug52cil.yi
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE199698 614 bp mRNA EST 26-JUN-2000 ug52c11.x1 Barstead bowel MPLRB9 Mus musculus cDNA clone IMAGE:1546004 3' similar to gb:X86374 M.musculus mRNA for TAG7 procesin (MOUSE); mRNA sequence.
                                                                                                                                           154 ValLysGlyHisArgAspValGlnSerThrLeuSerProGlyAspGlnLe 170
                                                                                                                                                                                                                                                                                                                   HisThrGlyProlleTrpAsnProMetSerlleGlyIleThrPheMetGl 120
lyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIleLysGlyAsp 103
               /clone="IMAGE:1546004"
/clone_lib="Barstead bowel MPLRB9"
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/dev_stage="8 weeks"
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                                                                                                                                                                                                                                                                                                                                                                       170 uTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182

    .614
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE199698
BE199698.1 GI:8711867
                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est1:BE199698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS BE199698
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JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                     104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
87
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AA238752 601 bp mRNA EST 03-MAR-1997
my35e09.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA
clone IMAGE:697864 5' similar to gb:X86374 M.musculus mRNA for TAG7
Not I and Eco RI sites of the modified pT7T3 vector. Source irradiated bowel harvested 72 hours after irradiation (1400 Gys). Library constructed by Bob. Barstead. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 ValGlnSerThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnSe 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alSerArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 GIGCAAAGCACTCTCTCTCCAGGIGACCAACTCTATCAGGTCAICCAAAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 IProAlaLysArgAlaLeuArgAlaAlaLeuAsnLeuLeuGluCysGlyV 143
                                                                                                                                                                                                                                                                                                                                         565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
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                                                                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                      26
                                                                        1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LeuLeuGlyLeuAlaThrSerCysSerPheIleValProArgSerGluTr
                                                                                                                                                                                                                                                                                                                         26 pargalaLeuProSerGluCysSerSerArgLeuGlyHisProValArgT
                                                                                                                                                                                                                                                                                                                                                                                           43 yrValValIleSerHisThrAlaGlySerPheCysAsnSerProAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 CysGluGlnGlnAlaArgAsnValGlnHisTyrHisLysAsnGluLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.688
                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: BE199698 from: 1 to:
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REFERENCE AUTHORS

FEATURES

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AA238564 591 bp mRNA basa basa musculus cDNA my35f04.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:697855 5' similar to gb:x86374 M.musculus mRNA for TAG7 protein (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled organs"
dev_stage="7 day"
/lab_host="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 591)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashO-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                   303
                                                                         heLeuIleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIle 100
                                                                                                                      353
                                                                                                                                                                    117
                                                                                                                                                                                                                 354 AAGGGTGACCACACAGGCCCATCTGGAATTCCATGTCTATTGGCATCAC 403
                                                                                                                                                                                                                                                               rPheMetGlyAsnPheMetAspArgVal.ProAlaLysArgAlaLeuArg 133
                                                                                                                                                                                                                                                                                                                                                          134 AlaAlaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 rAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL IMAGE Consortium (info@image.llnl.gov) for further
                                                                                               167 lyAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGly1leTh
                                                                                                                                                                                                                                                                                        404 CTTCATGGGGAACTTCATGGACCGGGTACCCG...CAAAGGGCCCTCCGT
                           GCAGCATTACCACAAGAATGAGCTGGGCTGGTGCGATGTAGCCTACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:697855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain-"FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA238564
AA238564.1 GI:1862588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est1:AA238564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:431415
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                    101
                           254
                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'); double-stranded cDNA was ligated to Eco RI adaptors [GTTGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 61)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Gelsel,S., Kucaba,T., Lacy,M., Le.,, Martin,J., Morris,M., Schellenberg,K., Stepto,M., Tan,F., Underwood,K., Morris,M., Tan,F., Underwood,K., Morre,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:697864"
/clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                              Waterston, M. Manage EST Project
The WashU-HHMI Mouse EST Project
Onpublished (1996)
Contact: Marra Manuse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 ATGTTGTTTGCCTGTGCTCTCTTGCCCTCCTGGGTCTGGCAACCTCCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSerCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 sSerPheIleValProArgSerGluTrpArgAlaLeuProSerGluCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 erSerArgLeuGlyHisProValArgTyrValValIleSerHisThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 lGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 183
Gaps: 2
Percent Identity: 96.175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 499.
Location/Qualifiers
1. .601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="mixed"
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5.126
97.814
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US-09-462-625-2 x AA238752
musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:431424
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source
ORGANISM
                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
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ORIGIN

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134 AlaAlaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSe 150
                                                                                                                                                                                                                                                               150 rAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProG 167
                                                                                                                                                                                                                                                                                                                                                                           67 lGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnP 84
                                                                                                                                   17 sSerPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysS 34
                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 95.628
                                                                                    Gaps:
                                                                              Length:
                                                                                                                         to: 591
                                                                                                                         from: 1
                                                                             897.00
5.039
97.268
                                                                                                                        Align seg 1/1 to: AA238564
                                                                                                       alignment_block:
US-09-462-625-2 x AA238564
                                                                              Quality:
Ratio:
Percent Similarity:
                                                                         alignment_scores
                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                               167
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 17, 2001, 07:48:37 ; Search time 14.4 Seconds (without alignments) 962.762 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-462-625-2 996 1 MLFACALLALIGLATSCSFI.....TLSPGDQLYQVIQSWEHYRE 182 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		hypothetical prote	Ħ	N-acetylmuramoyl-L	tms1 protein - mou	hypothetical prote	lysyl endopeptidas	osteonidogen - hum		hypothetical prote	nitrogenase (EC 1.	hypothetical prote	arginine-specific	ciml protein homol	arginyl endopeptid	gingipain R (EC 3.	gingipain R (EC 3.	probable hemagglut	hypothetical prote	ferrichrome-iron r	beta-lactamase exp	·			hypothetical 40.1	hypothetical prote	ú		hypothetical prote
SUMMARIES	Œ	G70520	T35303	MUBPA7	S07506	S54144	G83443	C69233	G00043	T26751	T33375	S34945	н96689	S41406	T09041	I40229	S49763	A55426	E83641	S76310	S74447	E83080	WZBEB6	G72522	T34767	D65096	н85968	D82388	VCBW	A83038
	DB :	~	~	-	7	~	~	7	~	~	~	~	~	~									-		~	7	7		-	~
	å Query Match Length DB	539	308	151	151	44	702	445				526	726	234	276	991	1526	1704	3535	416	863	188	3421	298	242	356	356	929	260	405
•	Query Match	20.3	13.1	11.9	11.9	10.4	8.4	7.9	7.9	7.8	7.8	7.7	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.2	7.2
•	Score	201	130	119	118.5	104	84	79	78.5	78	77.5	77	75.5	74.5	74.5	74.5	74.5	74.5	74.5	74	74	73.5	73.5	73	72.5	72.5	72.5	72.5	72	72
	Result No.		7	m	4	2	Q	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	29

TS503 TS502 TS503 TSF7.14c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T33303 TS503 TS503 TS503 TS503 TS503 TS504 TS5

probable disease r apolipoprotein(a)	conserved hypothet	thermophilic desur	endopeptidase La (hypothetical prote	DNA-directed DNA p	alpha-amylase (EC	nitrogenase iron-m	nifE protein - Met	nitrogenase (EC 1 .	lysostaphin precur	lysostaphin precur	alpha-galactosidas	hypothetical prote	probable zinc prot
T05259 T18518	Н82645	JC7231	A36895	T20492	JDVLVA	S23257	н69075	T10095	B32057	A25881	801079	S74219	A96758	T30090
00	7	N	٦	7	Н	~	7	7	7	7	7	7	~1	7
835 2869	357	454	827	827	832	477	478	483	518	389	480	746	779	845
7.2	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
72	7.1	71	7.1	71	71	20	70	70	70	69.5	69.5	69.5	69.5	69.5
. 30	32	33	34	35	36	37	38	36	40	4.1	4.5	43	44	4.5

ALIGNMENTS

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tmsl protein - mouse
tmsl protein - mouse
(c)Species: Mus musculus (house mouse)
c)Species: Mus musculus (house mouse)
c)Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
C;Accession: 554144
R;Kustikova, O.S.
submitted to the EMBL Data Library, April 1995
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A;Accession: 554144
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 R-----VPAK-RALRAALNLLECGVSRGFLRSNYE---VKGHRDVQSTLSPGDQLYQV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 KGKFDANFTPAQMQSLRSLLVT-----LLAKYEGSVLRAHHDVAPKACPS---FDL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 RNVQHYHKNELGWCDVAXNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFWD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                           65 RNVQHYHKNELGWCDVAXNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMD 124
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-151 <BEC>
A;Cross-references: EMBL:X17255; NID:915682; PIDN:CAA35133.1; PID:915695
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R;Beck, P.J.; Gonzalez, S.; Ward, C.L.; Molineux, I.J.
J. Mol. Biol. 210, 687-701, 1989
A;Title: Sequence of bacteriophage T3 DNA from gene 2.5 through gene A;Reference number: S07500; MUID:90133923
A;Accession: S07506
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                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - phage T3
N;Alternate names: gene 3.5 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: phage T7 N-acetylmuramoyl-L-alanine amidase C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%; Score 118.5; DB 2;
nilarity 30.4%; Pred. No. 0.00027;
Conservative 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.4%; Score 104; DB 2; Similarity 95.5%; Pred. No. 0.0016; 21; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                  125 R-----VPAK-RALRAALNLLECGVSRGFLRSNYEV 154
                                                                                                                                                                                                                                                                                                Score 119; DB 1;
Pred. No. 0.00024;
                                                                                                                     18; Mismatches
                                                                          11.9%;
33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-44 <KUS>
A;Cross-references: EMBL:X86374
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 38; Conserv
                                                                          Ouery Match
Best Local Similarity
Matches 33; Conserv
     C; Keywords: hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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A;Residues: 1-38, E' 40-118, 'V',120-151 <DUW>
A;Cross-references: EMBL:V01146; NID:9431187; PIDN:CAA24403.1; PID:9431190
C;Comment: This late gene protein is not required for lysis but plays an important role
11y bound. The functional significance of this is not clear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ge
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A; Mesidues: 1-151 cDU2>
R; Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A; Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7
A; Reference number: 542283; MUID:83241725
A; Accession: 542302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-151 <DU1>
R;Dunn, J.J.; Studier, F.W.
A;Mol. elol. 148, 303-330, 1981
A;Title: Nuclectide sequence from the genetic left end of bacteriophage T7 DNA to the language number: A92866; MUID:82078034
A; Reference number: 221574
A; Accession: T35303
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 1.308 <SEE>
A; Cross references: EMBL.AL096872; PIDN:CAB51271.1; GSPDB:GN00070; SCOEDB:SC5F7.14c
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB:SC5F7.14c
                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: T7 lysozyme
C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 18-Jun-1999
C;Accession: C94615; D92866; S42302; S43502; A01001
R;Dunn, J.J.; Thompson, K.
A;Reference number: A94615
A;Reference number: A94615
A;Reference number: A94615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPAKRALR-----AALNILECGV-----SRGFLRSNY------EVKGHRDV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 NELG---WCDVAYNFLIGEDGHVYEGRGWNI----KGDHTGPIWNPMSIGITFMGNFMDR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 VPVPDELTDAIAAVAAWKLGETGTDPRAKVALVSSNGL--SRYAAGATAMLPAVAGHEDG 280
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                             20 IVPRSEW----RALPSECSSRLGHPVRYVVISHTAGSFCNSPD--SCEQQARNVQHYHK 72
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.5%; Pred. No. 4.7e-05;
Matches 56; Conservative 17; Mismatches 67; Indels
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acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - phage T7

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Map position: 26.77-27.90 superfamily: phage T7 N-acetylmuramoyl-L-alanine amidase

A; Molecule type: DNA A; Residues: 1-38, 'E', 40-151 <DUN> A; Cross-references: EMBL:V01146 R; Dunn, J.J.; Studier, F.W. submitted to the EMBL Data Library, October 1993 A; Reference number: \$43501 A; Accession: \$43502

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A; Molecule type: mENA
A; Residues: 1-1376 < OHN>
A; Cross-references: GB:D86425; NID:91449166; PIDN:BAA13087.1; PID:91449167
C; Superfamily: nidogen; EGF homology; LDL receptor YWTD-containing repeat homology;
F; 806-843/Domain: EGF homology < EGF1>
F; 853-891/Domain: EGF homology < EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL023839; PIDN:CAA19506.1; GSPDB:GN00021; CESP:Y39A1C.4
A;Experimental source: clone Y39A1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26751
                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: G00043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              876 FSCACLPGYAGDGHOCTDV------DECSENRCHPA--ATCYNTPGSFSCRCQPGY 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     924 YGDGFQCIPDSTSSLIPCEQQQRHAQAQYAYPGARFHIPQCDEQGNFLPLQCHGSTGFCW 983
                                                                                                                                76 GMYGADAVIYAGHGGYMAGHYDGRGGNATPPFGLVARDGYIWSAGDMMWVNGTTFYAPFK 135
                                                                              ----IWNP----MSIGITFMGNFM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
3 FACALL-ALLGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSF---CNS-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;941-1006/Domain: thyroglobulin type I repeat homology <THY1>F;1020-1085/Domain: thyroglobulin type I repeat homology <THY2>F;1242-1286/Domain: LDL receptor YWTD-containing repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PDS----CEQQARNVQHYH-----KNELGWCDVAYNFL---
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.9%; Score 78.5; DB
Best Local Similarity 25.2%; Pred. No. 27;
Matches 38; Conservative 10; Mismatches
                                                                                                                                                                                                                         984 CVDPDGH-----EVPGTQTPPGSTPPHCG 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 -IGEDGHVYEGRGWNIKGDHTGPIWNPMSIG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1998
A;Reference number: 220259
                                                                                   ---GEDGHVYEGRGWNIKGDHTGP-----
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A; Introns: 65/3; 203/3; 320/3; 372/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ohno, I. submitted to GenBank, July 1996 A;Reference number: H00043 A;Accession: G00043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: Y39AlC.4
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G00043
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-oct-1999
C;Accession: C69233
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J; Bacteriol. 179, 7135-7155, 1997
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A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                     Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
Affilte, Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A82956, MUID: 20437337
A;Accession: 683443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA A. Molecule type: DNA A. Molecule type: DNA A. Molecule type: DNA A. Cross 1.702 <STO> A. Cross-references: 1.702 <STO> A. Cross-references: STAEO04589; GB: AEO04091; NID: 99947574; PIDN: AAG05002.1; GSPDB:GN001 A. Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
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A;Accession: C69233
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                               RESULT 6
G83443
hypothetical protein PA1613 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- MGNFMD--- 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 EWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHKNELGW---CDVA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
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3.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 84;
Pred. No.
                              1 MLFACALLALLGLATSCSFIVP 22
                                                          8.4%;
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Best Local Similarity 24.0°
Matches 43; Conservative
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A; Residues: 1-445 <MTH>
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A;Start codon: GTG
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Length 424;

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Score 78;

7.88;

Query Match

-- QHYHKNELGWCDVAYNFLI- 86

34 SSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNV---

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RESULT 13
S41406
arginine-specific cysteine proteinase - Porphyromonas gingivalis
c;Species: Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C;Accession: S41406
E;Sotiropoulos, C.; Kirszbaum, L.; Slakeski, N.; Jackson, C.; Reynolds, E.
Submitted to the EMBL Data Library, January 1994
A;Description: Complete nucleotide sequence of the prtR gene encoding an arginine-spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon R; Theologis, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chun, C.W.; Chun, C.B.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Hunbers: Hunber, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Atthors: Hunber, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Atthors: Hunber, J.L.; Zakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A; Thile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE005173; NID: 911054539; PIDN: AAG27838.1; GSPDB: GN00141
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-234 <SOT>
A;Residues: 1-234 <SOT>
A;Cross-references: EMBL:Z29570; NID:g450920; PIDN:CAA82674.1; PID:g450921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F28G11.16 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: H96689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 645 YGCVTLHIECLIGKDLYMKPGSSWLFKGRKVRVLNNHRWTRPICRECKDRCPHXIVFRR 704
                                                                                                                                                                                                                116 CNSPGFAGPSQSG--GHHKINIAWLNORVGTVEPDYLGEHVINYVGE-YNIQGDQEVMID 222
                                                                                                                                                              54 CNSPDSCEQQARNVQHYHKNELGWCDVAYNFL----IGEDGHVYEGRGWNIKGDHTGPI- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPSECSS-----RLGHPVRYVVISH-----TAGSFCNSPDSCEQQAR-NVQHYHKNE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                588 ALCFKCAAIPQKVRYKHDNHVLILSYGKEIETSTMAYWC---EACERKINPKGOFYNCDE
                                                                                                                                                                                                                                                                                                                                                                     223 YFNRMGIQVLSTFTGN--GSYDSLRMMHRAHLNVLECARSAEYICDELRARYGI 274
                                                                                                                                                                                                                                                                                                                            109 -WNPMSIGI--TFMGNFMDRVPAKRAL-RAALNLLECGVSRGF----LRSNYEV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 726;
        Length 526;
*, ccore 77; DB 2;
%; Pred. No. 12;
15; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6%; Score 75.5; 1
24.2%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.6 Best Local Similarity 24.2 Matches 32; Conservative
                        Query Match 7.7%
Best Local Similarity 30.7%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 AALNLLECGVSR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLNFCSTGCMR 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-726 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: F28G11.16
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain C;Superfamily: ATP; nitrogen fixation; oxidoreductase C;Keywords: ATP; nitrogenase vanadium-iron protein alpha chain homology <VIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA; Molecule type: DNA; PResidues: 1-699 CABC; PResidues: 1-699 CABC; PROSIGES: 1-699 CABC; PROSIGES: 1-699 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 CABC; PROSIGES: 1-690 C
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C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T33375
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                                                                                                                                                                                                                                                                                                                                                                                                                                120 GNFMDRVPAKRALR----AALNLLEC--GVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PGNRIYEL 279
                                                                                                                                                                                                                                                                          QARNVQHYHKNELGWCDVAYNFLIGEDGHVYEG---RGWNIKGDHTGPIWNPMSIGITFM 119
                                                                                                            LLGLATSCSFIVPRSEWRAL-----PSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCYIPHSEAKSFENAQKSCEEECGNLVSIHSANENLYLNILAYNFLPGE--YIYIG 221
                                                                                                                                                                                                                                                                                                                        43 YVVISHT-AGSFCNSPDSCEQQARNVQHYHK-NELGWCDV-AYNFLIGEDGHVYEG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Beck, C.; O'Brien, D.; Kramer, J.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid T07H3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                     72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 AMSMETMIEGRPLAGNYPVTSELLQCTPPLDLGFTATGCKF--
                                                                                                                                                                                               LWNYAEDLDIYLPRSTWMILRNFRNVWGSSAWKGADGPARY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 7.8%; Score 77.5; Di Local Similarity 41.1%; Pred. No. 15; hes 23; Conservative 10; Mismatches
No. 7.5;
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 65/3; 159/1; 384/1; 537/3; 600/3
        Pred.
                                         56;
20.6%;
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: Z21332
        Similarity
39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 | 1::
280 IN--EMYQK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 IQSWEHYRE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T33375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position:
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    Best Local
Matches 3
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Arch. Biochem. Brophys. 316, 917-925, 1995
A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine A;Reference number: I40229; MUID:95168884
A;Accession: I40229
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T09041
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrd bubmitted to the Protein Sequence Database, June 1999
A;Reference number: 216533
A;Accession: T09041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arginyl endopeptidase - Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40229
                                                                                                                                                                                                                                                                                                                                                         cim1 protein homolog F26K10.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 FMGNFMDRVPAK--RALRAALNLLE------CGVSRGFLRSNYEVKG------H 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                            .----н 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HVYEGR 96
                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:D26470; NID:9927644; PIDN:BAA05484.1; PID:9927645
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 NWCIIG---GPLKGPFSIKLTTLSAERNRVTAGRRMETVRKVHPNQRLLRSLLFLL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PAKRALRAALNLL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL049803; GSPDB:GN00062; ATSP:F26K10.130
A;Experimental source: cultivar Columbia; BAC clone F26K10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 276;
                          Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                            118 FMGNFMDRVPAK--RALRAALNLLE------CGVSRGFLRSNYEVKG---
                                                                  Indels
                                                               27;
                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                     ; Score 74.5; DE; Pred. No. 8.1; 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 7.5%; Score 74.5; Di
Best Local Similarity 27.6%; Pred. No. 9.8;
Matches 32; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SCEQOARNVQHYHKNELGWCDVAYNFLIG-EDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GWNIKGDHTGPIWNPMSIGITFMGNFMDRV----
                                                                                                                                                                                                                              KDIPAKITPGIKSDQVYGQIVGNDHYNE 116
                                                                                                                                                                                                      158 RDVQSTLSPG---DQLYQVIQSWEHYRE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ATSP:F26K10.130
A;Map postition: 4
A:Introns: 54/1; 154/2; 197/3; 235/1
C;Superfamily: expansin
                          7.5%;
26.1%;
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                                                                    Conservative
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Best Local Similarity
Matches 23; Conserva
                          Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-276 <BEV>
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Oy 158 RDVQSTLSPG---DQLYQVIQSWEHYRE 182
:1::::|| ||:| :|:|
Db 307 KDIPAKITPGIKSDQVYGQIVGNDHYNE 334
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Search completed: December 17, 2001, 07:49:02 Job time: 25 sec

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December 17, 2001, 07:48:37 ; Search time 11.77 Seconds (without alignments) 566.950 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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US-09-462-625-2 996 1 MLFACALLALLGLATSCSFI.....TLSPGDQLYQVIQSWEHYRE 182 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

100059 segs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		P20331 bacteriopha		rhod			P28784 porphyromon	_		7		Q13510 homo sapien					P16266 azotobacter					P37458 salmonella	P08516 rattus norv	treponem	Q9w6s5 xenopus lae			homo sapi	P27050 bacillus ci	daucus c	xenopus 1	9125	P40009 saccharomyc
di .	NAAA_BPT7	NAAA_BPT3	NID2_HUMAN	ANFD_RHOCA	GSHH_PIG	CPG2_PORGI	CPG1_PORGI	TEGU_HSVEB	YGJJ_ECOLI	COAT_SBMV	ANFD_HELGE	ASAH_HUMAN	LON2_MYXXA	DPOL_HPBVY	NIFE_METTH	NIFE_METMP	ANFD_AZOVI	AMY_ALTHA	GSHH_MOUSE	LSTP_STAST	LSTP_STASI	WECF_SALTY	CP41_RAT	Y483_TREPA	ALC_XENLA	GDNR_RAT	ZAN_MOUSE	GSHH_HUMAN	CHID_BACCI	CCBS_DAUCA	- 1	GLGA_BACSU	YND1_YEAST
DB	-	-	-	Н	- 1	Н	7	Н	Н	 1	-	٦	~	-	-	Н		-													-		-
Length DB	150	150	1375	526	197	736	991	3421	356	279	280	395	826	832	478	483	518	699	197	480	493	426	509	374	389	468	5376	197	524	579	428	484	630
>4		11.9		7.7	7.7	7.5	7.5	7.4	7.3	7.2	7.2	7.2	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.8	6.8	6.8	6.8	9.9	6.7	6.7	6.7
Score	121	118.5	78.5	77	•	4	4	73.5	ď		72	72	71	71	70		70	70	σ.	69.5	σ	69	69	68.5	68.5	68	68	67.5	67.5	67.5	67	67	29
Result No.	1	7	e	4	'n	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P29476 rattus norv P34881 arabidopsis Q89438 2 genome po Q38135 bacteriopha P19693 bacteriopha P38487 saccharomyc P19728 bacteriopha P77432 escherichia P31797 bacteriopha P3797 bacteriopha P3797 bacteriopha P3797 bacteriopha P379484 hepatitis b
MOSI_RAT MTDM_ARATH POIG_ZYMVR ALYS_BPRIT VCAA_BPT3 YBRIL_YEAST VCAB_BPT3 YDEV_ECOLI CDGT_BACST HEXB_ALISO LOM_BUCAI DPOM_HPBVY
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1429 1534 3083 270 347 376 4433 530 711 777
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ALIGNMENTS

150 AA

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CATALYTIC ACTIVITY: HYDROLYZES THE LINK BETWEEN N-ACETYLMURAMOYL RESIDUES AND L-AMINO ACID RESIDUES IN CERTAIN BACTERIAL CELL-WALL
                                                                                                                                                                        STRAIN-LURIA;
MEDILINE-90133923; PubMed-2614843;
MEDILINE-90133923; PubMed-2614843;
MEDILINE-90133923; PubMed-2614843;
Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
J. Mol. 19.01. 210:687-701(1989).
I. MOL. 110: PROTEIN IS NOT REQUIRED FOR LYSIS BUT PLAYS AN INPORTANT ROLE IN DNA SYNTHESIS. IT IS KNOWN TO DETACH THE HOST CHROMOSOME FROM THE BACTERTAL MENARANE TO WHICH IT IS NORMALLY CHROMOSOME FROM THE BACTERTAL WHILLY CHROMOSOME BONDS IN THE BACTERIAL CELL WALL AND BINDS TO AND INHIBITS TRANSCRIPTION BY TARN POLYMERASE (BY SIMILARITY).
                                                                                                           Viruses; dsĎNA viruses, no RNA stage; Tailed phages; Podoviridae;
T7-like phages.
                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28) (T3 LYSOZYME).
                              STANDARD;
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130 1
150 AA;
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                                                                                                                                        NCBI_TaxID=10759;
                                                                                                          Bacteriophage T3
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: ZINC (REQUIRED ONLY FOR AMIDASE ACTIVITY).
ENZYME REGULATION: BINDING OF T7 RNA POLYMERASE INHIBITS AMIDASE
                                    SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
                                                                                                                                                                                                                                                                                             ZINC (TO THE HYDROXYL GROUP OF TYR THROUGH A WATER MOLECULE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 150;
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-> G (IN REF. 1, 2 AND 2)
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ilarity 34.7%; Pred. No. 5.8e-05;
Conservative 16; Mismatches 38
                                                                                                                                                                                              PIR; A01001; MUBPA7.
PIR; A01001; 44202.
PIR; 542302.
PDB; LLBA; 30-APR-94.
PDB; LARO; 21-OCT-98.
Interpro; IPR002502; Amidase_2.
PF01510; Amidase_2: 1.
Pffam; PF01510; Amidase_2: 1.
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ZINC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 R-----VPAK-RALRAALNILECGVSRGFLRSNYE---VKGHRDVQSTLSPGDQLYQV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 RNVQHYHKNELGWCDVAXNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMD 124
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                                        (BY SIMILARITY)
--- ENZYME REGULATION: BINDING OF T3 RNA POLYMERASE INHIBITS AMIDASE
ACTIVITY (BY SIMILARITY)
--- SIMILARITY: BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
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ZINC (BY SIMILARITY).
ZINC (TO THE HYDROXYL GROUP OF TYR
THROUGH A WATER MOLECULE) (BY
SIMILARITY).
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-!- COFACTOR: ZINC (REQUIRED ONLY FOR AMIDASE ACTIVITY)
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ZINC (BY SIMILARITY).
812C1DFF80F474FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 118.5; DB 1; 30.4%; Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P00806; ILBA.
InterPro; IPR002502; Amidase_2.
Pfam, PF01510; Amidase_2; 1.
Hydrolase; Late protein; Zinc, INIT_MET 17 17 ZINC METAL 46 46 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16743 MW;
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Best Local Similarity 30.4%
Matches 38; Conservative
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125 R-----VPAK-RALRAALNLLECGVSRGFLRSNYEV 154

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Cancellous bone:
Ohno I., Hashimoto J., Takaoka K., Ochi T., Okubo K., Matsubara K.;
"The clouing and characterization of a cDNA for the novel bone matrix protein: osteonidogen.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          Kohfeldt E., Sasaki T., Goehring W., Timpl R.;
Kohfeldt E., Sasaki T., Goehring W., Timpl R.;
Nidogen-2: a new basement membrane protein with diverse binding
properties.";
J. Mol. Biol. 282:99-109(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohno I., Okubo K., Matsubara K.; "Human osteonidogen gene: intron-exon junctions and chromosomal
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
MEDLINE-98406162; Pubmed-9733643;
                                                                                                                                             NID2_HUMAN STANDARD; PRT; 1375 AA. 014112; 043710; 15-DEC-1998 (Rel. 37, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) NIDOGEN-2 PRECURSOR (NID-2) (OSTEONIDOGEN).
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AB009799; BAA24112.1; -.
AB009778; BAA24112.1; JOINED.
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AB009789;
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                      174 IQSWE 178
                                                       136 KRWWE 140
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DT 20-ADG

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OC Mammal

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EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4.

EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).

THYROGLOBULIN TYPE 1 1.

THYROGLOBULIN TYPE 1 2.

LDL-RECEPTOR YWTD MOTIF 1.

LDL-RECEPTOR YWTD MOTIF 2.

LDL-RECEPTOR YWTD MOTIF 3.

LDL-RECEPTOR YWTD MOTIF 4.

LDL-RECEPTOR YWTD MOTIF 5.
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MWTMISPPTSRPSPLEWRISTRATAEAESCTERTPPPQCWA
WPPAMCALASRALRAFYPHPRLPGHLGAGRRLRGGGTR
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PROSITE; PS000484; THYROGLOBULIN_1; 2.
PROSITE; PS010486; EGF_04, 4.
PROSITE; PS01187; EGF_04, 2.
Basement membrane; Extracellular matrix; Glycoprotein; Signal; Calcium-binding; Repeat; EGF_1ike domain; Cell adhesion.
SIGNAL. 31 1375 NIDOGEN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> G (IN REF. 1).
414299D244205FBC CRC64;
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                                                                                                                                                                                                                                                                                                            Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR000561; EGF-like.
Interpro; IPR000561; EGF-like.
Interpro; IPR000033; Ldl_rcptor_rep.
Interpro; IPR001033; Ldl_rcptor_rep.
Interpro; IPR001036; Interpro; IPR001061; Interpro; IPR001068; EGF, 5.
Pfam; PF00068; EGF, 5.
Pfam; PF00068; Idl_rccpt_b; 4.
Pfam; PF00068; Idl_rccpt_b; 4.
SMART; SM00179; EGF_CA; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00139; LN; CA; 2.
SMART; SM00139; LY; 2.
SMART; SM00139; IX; 4.
JOINED.
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JOINED.
                                                            BAA24112.1; JOINED.
BAA24112.1; JOINED.
BAA24112.1; JOINED.
                                                                                                                                                      AB009795; BAA24112.1; JOINED.
AB009796; BAA24112.1; JOINED.
AB009797; BAA24112.1; JOINED.
AB009798; BAA24112.1; JOINED.
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1375 AA;
                                                                                                                                                                                                 EMBL; AB009796;
EMBL; AB009797;
      AB009790;
                                                                                                                                  EMBL; AB009794;
                                                                                                                                                                EMBL; AB009795;
                                        AB009791;
                                                                                                                                                                                                                                                                                           MIM; 605399;
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                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 FSCACLPGYAGDGHQCTDV-----DECSENRCHPA--ATCYNTPGSFSCRCQPGY 922
                                                                                                                                                             923 YGDGFQCIPDSTSSLIPCEQQQRHAQAQYAYPGARFHIPQCDEQGNFLPLQCHGSTGFCW 982
                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1) (NITROGENASE
COMPONENT I) (DINITROGENASE 3 ALPHA SUBUNIT).
                               Gaps
                                                           3 FACALL-ALLGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSF---CNS-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: IRON-SULFUR.
SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO DELTA CHAINS.
SIMILARITY: BELONGS TO THE NIFD/NIFR/NIFE/NIFN FAMILY.
                                                                                                                               ------PDS-----CEQQARNVQHYH-----KNELGWCDVAYNFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schueddekopf K., Hennecke S., Liese U., Kutsche M., Klipp W., "Characterization of anf genes specific for the alternative nitrogenase and identification of nif genes required for both
Length 1375;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00148; oxidored_nitro; 1.
PROSITE; PS00090; NTTROGENASE_1_2; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Iron-sulfur.
SEQUENCE 526 AA; 59061 MW; D6AD51EA40421074 CRC64;
                               46;
 DB 1;
                                                                                                                                                                                                                                                                                                                      526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxidored_nitrognse_1.
7.9%; Score 78.5; Di
25.2%; Pred. No. 9.9;
tive 10; Mismatches
                                                                                                                                                                                                                                 983 CVDPDGH-----EVPGTQTPPGSTPPHCG 1006
                                                                                                                                                                                                 86 -IGEDGHVYEGRGWNIKGDHTGPIWNPMSIG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93323746; PubMed-8332060;
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X70033; CAA49625.1; -. PIR; S34945; S34945. HSSP; P00467; 1MIO.
                   Best Local Similarity 25.29
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-1061;
                                                                                                                                                                                                                                                                                                                     ANFD_RHOCA
Q07933;
 Query Match
                                                                                                                                                                                                                                                                                                          ANFD_RHOCA
                                                                                                                                    57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schuckelt R., Brigelius-Flohe W., Foveri A., Reumkens J., Strassburgelt R., Ursini F., Wolf B., Flohe L., Strassburgel W., Ursini F., Wolf B., Flohe L., Flohe L., Phospholipid Mydroperoxide glutathione peroxidase is a selencenzyme distinct from the classical glutathione peroxidase as evident from cDNA and animo acid sequencing."

Free Radic. Res. Commun. 14:343-361(1991).

Free Radic. Res. Commun. 14:343-361(1991).

TOXICITY OF INGESTED LIPID HYDROPEROXIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL AND CYTOPLASMIC.
-!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS
-!- BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
                                    CNSPGFAGPSQSG--GHHKINIAWINQKVGTVEPDYLGEHVINYVGE-YNIQGDQEVMID 222
CNSPDSCEQQARNVQHYHKNELGWCDVAYNFL----IGEDGHVYEGRGWNIKGDHTGPI- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93312346; PubMed=8323565; Sudimoto M.; Sudimoto M.; Sudimoto M.; Sudide R.A., Dyer J.A., Moran T., Evenson J.K., Sugimoto M.; Sunde R.A., Dyer J.A., Moran T., Evenson J.K., Sugimoto M.; Phospholipid hydroperoxide glutathione peroxidase: full-length pig blastocyst cDNA sequence and regulation by selenium status."; Biochem. Biophys. Res. Commun. 193:905-911(1993).
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE, MITOCHONDRIAL
PRECURSOR (EC 1.11.1.9) (PHGPX) (GPX-4).
                                                                                                223 YFNRMGIQVLSTFTGN--GSYDSLRMMHRAHLNVLECARSAEYICDELRARYGI 274
                                                                            -WNPMSIGI--TFMGNFMDRVPAKRAL-RAALNLLECGVSRGF----LRSNYEV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUTATHIONE + 2 H(2)0.
-1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE ENCODED BY THE OPAL CODON, UGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)0(2) - OXIDIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 40-197 FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Heart;
MEDLINE-92137773; PubMed-1778506;
                                                                                                                                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L12743; AAA31099.1; -.
EMBL; L12743; AAA31098.1; -.
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                      GSHH_PIG
P36968;
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Gaps

18;

Indels

46;

15; Mismatches

Query Match 7.7% Best Local Similarity 30.7% Matches 35; Conservative

7.7%; Score 77; DB 1; Length 526; 80.7%; Pred. No. 4.7;

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Query Match
Best Local S
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ikehara
                                                                                                                                                                                                                                                                                                                         CPG1_PORGI
                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 CNSPDSCEQQARNVQHYHKNELGW-----CDVAYNFLIGEDGHVYE-GRGWNIK---- 101
                                                                                                                                                                                                                                                                                                                           73 CGKTEVNYTQLVDL-HARYAECGLRILAFPCNQFGRQEPGSDAEIKEFAAGYNVKFDMFS 131
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                            16 CGTLAVPGLAGTMCA---SRDDWRCARSMHEFSAKDIDGHMVNLDKYRGYVCIVTNVASQ 72
                                                                                                                                                                                                                                                                53
                                                                              PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_2: 1.
Oxidoreductase; Peroxidase; Selenium; Selenocysteine;
Mitochondrion; Transit peptide; Alternative initiation.
TRANSIT 1 ? PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
CHAIN ? 197 PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE
                                                                                                                                        PEROXIDASE, MITOCHONDRIAL ISOFORM. PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE, CYTOPLASMIC ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GINGIPAIN R2 PRECURSOR (EC 3.4.22.37) (GINGIPAIN 2) (ARG-GINGIPAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potempa J., Mikolajczyk-Pawlinska J., Brassell D., Nelson D., Thoegersen I.B., Enghild J.J., Travis J., "Comparative properties of two cysteine proteinases (gingipains R) the products of two related but individual genes of Porphyromonas
                                                                                                                                                                                                                                                               5 CALLALLGLA-TSCSFIVPRSEWRALPS--ECSSR--LGHPVR-----YVVISHTAGSF
                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                          Length 197;
                                                                                                                                                                                                                                            57; Indels
                                                                                                                                                                      28 FOR CYTOPLASMIC ISOFORM. 73 22290 MW; 348645ABE35A7FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group; Bacteroidaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gingivalis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESIDUES IN P2 AND P3.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C25.
                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 230-651
                                                                                                                                                                                                                       Query Match
7.7%; Score 76.5; Di
Best Local Similarity 27.7%; Pred. No. 1.8;
Matches 41; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gingivalis (Bacteroides
                                                                                                                                                                                                                                                                                                                                                 102 ----GDHTGPIWNPMSI---GITFMGN 121
                                                                                                                                                                                                                                                                                                                                                                     132 KICVNGDDAHPLWKWMKVQPKGRGMLGN 159
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                 InterPro; IPR000889; Glut_peroxdse.
Pfam; PF00255; GSHPx; 1.
PRINTS; PR01011; GLUTPROXDASE.
X76009; CAA53596.1; ALT_INIT.
X76008; CAA53595.1; ALT_INIT.
S80257; AABJ1327.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98370998; PubMed-9705298;
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                     197
                                                                                                                                                                                            197 AA;
                                 PIR; JN0608; JN060
HSSP; P00435; 1GP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; CFB g.
                                                                                                                                                     28
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73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR RGP2
                               JN0608;
                                                                                                                                                                                                                                                                                                                                                                                                                     CPG2_PORGI
P95493;
                                                                                                                                                                         INIT_MET
SE_CYS
SEQUENCE
                                                                                                                                   CHAIN
                                                                                                                                                      CHAIN
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or send an email to license@isb-sib.ch).
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ENZYME REGULATION: REQUIRES CYSTEINE FOR ACTIVATION AND CA(2+)
AND/OR MG(2+) FOR STABILIZATION. IT IS STIMULATED BY GLYCINE-
CONTAINING DIPEPTIDES. IT IS RESISTANT TO INHIBITION BY PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ninkory (2007) (2007) Peptidase_C25.
InterPro; IPR001769; Peptidase_C25; Dfam; PF01364; Peptidase_C25; Usinience; Hydrolase; Thiol protease; Calcium; Signal; Zymogen. SIGNAL BY SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural characterization of argingipain, a novel arginine-specific cysteine proteinase as a major periodontal pathogenic factor from Porphyromonas gingivalis."; Arch. Biochem. Biophys. 316:917-925(1995).
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-59168884; PubMed-7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 FMGNFMDRVPAK--RALRAALNLLE-----CGVSRGFLRSNYEVKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 228-290 AND 517-541
                                                                                                                                                                                                                                                                                                                GINGIPAIN R2.
15E8F9FC54FDB52D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group; Bacteroidaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 74.5; 1
26.1%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 KDIPAKITPGIKSDQVYGQIVGNDHYNE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 RDVQSTLSPG---DQLYQVIQSWEHYRE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92406812; PubMed=1527017;
                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                            229
736 GI
81003 MW;
                                                                                                                                                               EMBL; U85038; AAB41892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 228-270.
                                                                                                                                                                                                                                                                                                                  230 7
736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                        MEROPS; C25.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=837;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AWVPDHSWGGFEGGINRFYGGYRINDCTEIMLSLRQDSSLDDLQWWGDFTPDLGYVIPNT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 FYGELGVG----GYMDLEGENKHKYSDGTYIEGGLEMKYGSWFGLIYGEGWTVQADHDGN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWNP-----MSIGIT-FMGNFM--DRVPAKRALRAALNLLECGVSRGFLRS-NYEVKGH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GRGWNIKGDHTGP 107
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                                                                           89 DGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFL 148
                                                                                                                  65 DGVLVEGRAWTVAGSKSGEA--PCMVSIV-----ELPNKITYANSANALCCVFSRLYG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Rlattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                      Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 72.5; DB 1; Length 356; 19.4%; Pred. No. 8.4; ive 25; Mismatches 71; Indels 7
DB 1; Length 3421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROTEIN YGJJ. S1D6089E92848385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 RALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Complete proteome.
                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDVQSTLS----PGDQLYQVI-----QSWEHY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 RDIMTALKVONLSGNFRYSVTATPAGHHDESKAWLHF 202
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                               149 RSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYRE 182
                                                                                                                                                                                                      116 DSGFYMHPGDGFQSTQIPARQFFDGV--WKSRSE 147
                                             12; Mismatches
                       85;
    Score 73.5;
Pred. No. 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 -YHKNELGWCDVAYNFLIGEDGHVYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN YGJJ PRECURSOR
                                                                                                                                                                                                                                                                                                         YGJJ_ECOLI STANDARD; F
P42591;
01-NOY-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 356 E
356 AA; 40099 MW;
      7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U18997; AAA57880.1; -. EMBL; AE000390; AAC76114.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 19.4 nes 42; Conservative
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EcoGene; EG12721; ygjJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12 / MG1655;
        Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                        YGJJ OR B3079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                           RESULT 9
                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FMGNFMDRVPAK--RALRAALNLLE-----CGVSRGFLRSNYEVKG------H 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 YEGDIKDFVDWKNORGLRTEVKVAEDIASPVTANAIQOFVKOEYEKEGNDLTYVLLVGDH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; PF01364; Peptidase_C25; 1.
Virulence; Hydrolase; Thiol protease; Calcium; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367078 MW; 5075EFE4739BB7AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                    GINGIPAIN R1.
RT -> TK (IN REF. 2).
1; 03EE3F43CEBE2544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
            INHIBITORS IN HUMAN PLASMA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74.5; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 RDVQSTLSPG---DQLYQVIQSWEHYRE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|: ::|| ||:| || || || 334
307 KDIPAKITPGIKSDQVYGQIVGNDHYNE 334
                                                                                                                                                                                                                                                                                 InterPro; IPR001769; Peptidase_C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                108782 MW;
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                                                                                                                                                                                                                                             EMBL; D26470; BAA05484.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LARGE TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                   227
991
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SEQUENCE 3421 AA:
                                                                                                                                                                                                                                                                                                                                                                                                        264 2
991 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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P28955;
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RESULT 8 TEGU_HSVEB

CONFLICT

SIGNAL PROPEP

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Query Match Best Local \$

118 Matches

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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hermodson M.A., Abad-Zapatero C., Abdel-Meguid S.S., Pundak S., Rossmann M.G., Tremaine J.H.;
"Antho acid sequence of southern bean mosaic virus coat protein and its relation to the three dimensional structure of the virus.";
Virology 119:133-149(1982).
                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
COAT PROTEIN PRECURSOR (CAPP PROTEIN).
Southern bean mosaic virus (SBMY).
Viruses; ssRNA positive-strand viruses, no DNA stage; ·Sobemovirus.
                                                                                                                                                                                                                                                                         MEDLINE-88044510; PubMed-2823471;
Wu S., Rinehart C.A., Kaesberg P.;
"Sequence and organization of southern bean mosaic virus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN, INTERACTION WITH RNA.
DOMAIN, VIRION SHELL.
DOMAIN, PROJECTING.
-> D (IN STRAIN COWPEA).
-> I (IN STRAIN COWPEA).
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R DOMAIN, IN:
S DOMAIN, VII
P DOMAIN, PR(
V -> D (IN S'
T -> I (IN S'
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InterPro; IRR000937; Viral_coat.
Pfam; PF00729; Viral_coat; 1.
PRINTS; PR00233; ICOSAHEDRAL.
PROSITE; PS00555; ICOSAHEDRAL.
Coat protein; 3D-structure; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23021; AAA46567.1; -. PIR; A04218; VCBW. PIR; D33739; VCBWSC.
                                                                                                                                                                                                                                                                                                                                               Virology 161:73-80(1987)
                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
279
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245
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=12139
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                                               COAT_SBMV
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LOUGHESS T.M., Bishop P.E.;
Loughlist T.M., Bishop P.E.;
In diverse diazotrophs.";
In diazotrophs.";
In diverse diazotrophs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ---IGEDGHVYEGRGW------NIKGDHTGPIWNPMSIGITFMGNFMDRVP- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
11-UTL-1999 (Rel. 38, Last annotation update)
11-UTROGENASE IRON-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1) (NITROGENASE COMPONENT I) (DINITROGENASE 3 ALPHA SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ECSSRLGHPVRYVVISH-----TAGSFCNSPDSCEQQARNVQHYHKNELGWCDVAYNFL- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 72; DB 1; Length 279; 25.4%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9B1BD427642493C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Heliobacterium group; Heliobacterium.
NCBI_TaxID=2699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 TSRAITIALDINEVSEKR 215
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Best Local Similarity
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submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
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SIGNAL
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97115857; PubMed-8955159;
MCOT J., Gaertner S., Li C.M., Quintern L.E., Bernardo K., Levran O., Schnabel D., Desnick R.J., Schuchman E.H., Sandhoff K.;

"Molecular cloning and characterization of a full length complementary DNA encoding human acid ceramidase. Identification of the first molecular lesion causing Farber disease.";

J. Biol. Chem. 271:33110-33115(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 CNSPDSCEQQARNVQHYHKNELGWCD-----VAYNFLIGEDGHVYEGRGWNIKGDH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CNSPGFAGPSQSG--GHHKINIAWIDQKVGTVEPKITSDYVIN----YVGE-YNIQGDQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Churchill J.R., Wieland S.J., Hoffman S., Gallin E.K., Murphy P.M.; "A new gene family predicted by a novel human heart cDNA."; Mol. Biol. Cell 6:418-418(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wieland S.J., Hoffman S., Churchill J.R., Gallin E.K., Murphy P.M.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
ACID CERANIDASE PRECURSOR (EC 3.5.1.23) (ACYLSPHINGOSINE DEACYLASE)
(N-ACYLSPHINGOSINE AMIDOHYDROLASE) (AC) (PUTATIVE 32 KDA HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 TGPI--WNPMSIGI--TFMGNFWDRVPAKRAL-RAALNLLECGVSRGFLRSNYEVK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 EVMLDYFKRMGIQVLSTFTGN--GSYDDLRAMHRAHLNVLECARSAEYICNELEVR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 72; DB 1; Length 280; 27.6%; Pred. No. 7.2; tive 17; Mismatches 43; Indels
                         -i - SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                       280 280
280 AA; 31772 MW; CDF25376AF1056A1 CRC64;
                                                                                                                                                                                                                                                                                                                             pfam; PF00148; oxidored_nitro; 1.
PROSITE: PS00090; NITROGENASE_1_2; 1.
PROSITE: PS00699; NITROGENASE_1_1; 1.
Oxidoreductase; Nitrogen fixation; Iron-sulfur.
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Interpro; IPR000318; Nitrognse_compl.
Interpro; IPR000510; Oxidored_nitrognse_l.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Conservative
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                                                                                                                                                                                                                                                                                                                                     -1- PTM: N-GLYCOSYLATED.
-1- PTM: N-GLYCOSYLATED.
-1- DISEASE: DEFECTS IN ASAH ARE THE CAUSE OF FARBER'S DISEASE. THIS SPHINGOLIPID DISEASE IS CHARACTERIZED BY SUBCUTAMENGUE LIPID-LOADED SPHINGOLIPID DISEASE IS CHARACTERIZED BY SUBCUTAMENTIES, MARKED NODULES, EXCRUCIATING PAIN IN THE JOINTS AND EXTREMETIES, MARKED ACCUMULATION OF CERAMIDE IN LYSOSOMES, AND DEATH BY THREE YEARS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 LMLDKAPMLKVIVNSLKNMINTFVPSGKVMQVVDEKLPGLLGNFPGPFEEEBMKGIAAVTD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SCVALVLLAAAVSCAVAQHAPPWTEDCRKSTYPPSGPTYRGAVPWYTINLDLPPYKRWHE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHK 72
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                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: LYSOSOMAL.
-i- TISSUE SPECIFICITY: BROADLY EXPRESSED WITH HIGHEST EXPRESSION IN
                                                                                                                    J. BIOL. Chem. 270:11098-11102(1995).
-i- FUNCTION: HYDROLYZES THE SPHINGOLIPID CERAMIDE INTO SPHINGOSINE AND FREE FATTY ACID.
                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: N-ACYLSPHINGOSINE + H(2)O = A FATTY ACID SPHINGOSINE.
-i- SUBUNIT: HETERODIMER OF ONE ALPHA AND ONE BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                        Bernardo K., Hurwitz R., Zenk T., Desnick R.J., Ferlinz K., Schuchman B.H., Sandhoff K.; "Purification, characterization, and biosynthesis of human acid "Purification, characterization, and biosynthesis of human acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycoprotein; Lysosome; Signal; Disease mutation;
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18.1%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i - SIMILARITY: BELONGS TO THE ACID CERAMIDASE FAMILY.
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EMBL, AF220172; AAF91230.1; JOINED.
EMBL, AF220173; AAF91230.1; JOINED.
CHARACTERIZATION.
MEDLINE=95263420; PubMed=7744740;
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44649 MW;
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Best Local Similarity 18.1%
Matches 43; Conservative
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47 SHTAGSFCNSPDSCEQQARNVQH-
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-i- SUBGNIT: HOMOTETRAMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- DEVELOPMENTAL STAGE: EXPRESSED DURING BOTH VEGETATIVE GROWTH AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 175:4538-4544(1993).
-!- FUNCTION: DEGRADES SHORT-LIYED RECULATORY AND ABNORMAL PROTEINS.
ESSENTIAL FOR FRUITING BODY FORMATION AND DEVELOPMENT.
-!- CATALITIC ACTIVITY: HUPROLYSIS OF LARGE PROFEINS SUCH AS GLOBIN,
CASEIN AND DENATURATED SERUM ALBUMIN, IN PRESENCE OF ATP.
                                        110 ---NPMSIGITFMGNFMDRVPAKRALRAALNLLECGVSRGF-----LKSNYEVKG 156
                                                         180 EQLKPLITVNLDFQRN-----NTTVFKASSFAGYVGMLTGFKPGLFSLTLNERFSING 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENT.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
LON FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93322334; PubMed-8331082;
Gill R.E., Karlok M., Benton D.;
Myxococcus xanthus encodes ATP-dependent protease which is
required for developmental gene transcription and intercellular
                                                                                                                                                                                                                                                                                                                                 Tojo N., Inouye S., Komano T.; "The lond gene encoding an The lond gene is homologous to the lon gene encoding an ATP-dependent protease and is essential for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01046; LON_SER; 1.
Hydrolase; Serine protease; ATP-binding; Multigene family.
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcaceae
                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).
                                                                                                                                 826 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 175:4545-4549(1993)
                                                                                                                                                                                                                                                                                                                      MEDLINE-93322335; PubMed-8331083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001939; AAA_subfam.
InterPro; IPR003111; LON.
InterPro; IPR001984; Lon_endopep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00830; ENDOLAPTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13204; BAA02491.1; -. EMBL; L19301; AAA72018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003593; AAA.
                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A36895; A36895.
MEROPS; S16.003; -.
                                                                                                                                                                                                                             Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                             Myxococcus xanthus
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=34;
                                                                                                                                                                                                               LOND OR BSGA
                                                                                                                                  LON2_MYXXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                              P36774;
                                                                                                                     LON2_MYXXA
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Transferase; RNA-directed DNA polymerase; DNA-directed DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                      365 IKNDMRGPILCLVGPPGVGKTSLGQSVAKATGRKFVRLSL------GGVRDEAEIRG 415
                                                                                                                                                                                                                                                                                                          100 IKGDHTGPIW---NPMSIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTEIN (INCLUDES: DNA-DIRECTED DNA POLYMERASE (EC 2.7.7.7); RNA-DIRECTED DNA POLYMERASE (EC 2.7.7.7); RNA-DIRECTED DNA POLYMERASE H (EC 3.1.26.4)]
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- YHKNELGWCDVA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDLINE-SEND10201; PubMed-399327;
Gallbert F., Mandart E., Fitoussi F., Tiollais P., Charnay P.;
"Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase, Nuclease; Endonuclease; DNA replication; DNA-binding
SEQUENCE 832 AA; 93676 MW; 7AB3AAE58A57DOD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloned in E. coli.";
Nature 281:646-650(1979).
-!- CATALYTIC ACTIVITY: DEOXYNUCLEOSIDE TRIPHOSPHATE -
N PYROPHOSPHATE + DNA(N).
-!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-
                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus (subtype ayw).
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
NCBL_TaxID=10418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 71; DB 1; Length 832; 23.2%; Pred. No. 31; Live 18; Mismatches 38; Indels
                                                                                                                                                                                             Length 826;
                          GLU-RICH (ACIDIC).
ATP (POTENTIAL).
BY SIMILARITY.
F6765E0D91C948D8 CRC64;
                                                                                                                                                                                             DB 1;
30;
                                                                                                                                                                           7.1%; Scor. 27.5%; Pred. No. 30, 17.5%; Pred. No. 30, 17.4.e. 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 832 AA.
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InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVISe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V01460; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00242; DNA_pol_viral_C; 1. Pfam; PF00242; DNA_pol_viral_N; 1.
0
275 GI
385 AT
701 BY
90307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             157 HRDVQSTLSPGDQLYQVIQS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 HRRTYVGALPG----RFIOS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                           22; Conservative
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Matches 32; Conserv
                                                                                                                                                                                                                                Best Local Similarity
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P03156;
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and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 SIGITEMGNEW-DRVPAK--RALRAALNLLECGVSRGFLRSNYEVK------GHR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 QARNVQHYHKNELGW---CDVAYNFLIGE-DGHVYEGRGWNIKGDH--TGPIWNPM---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee H.-M., Dubois J.,
                                                      82 YNFLIGEDGHV---YEGRGWNIKGDHTGPIWNPMSI---GITFMGNF-----MDRVPA 128
                                                                                          ---LOSQQGHLARRQQGRSWSIRAGFHPTARRPFGVEPSGSGHTTNFASKSASCLHQSPV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith D.R., Doucette-Tamm L.A., Deloughery C., Lee H.-M., Dubois J Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Reagle P., Lumm W., Pothier B., Olu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J Bacteriol. 179:7135-7155(1997).

- I- FUNCTION: THIS PROTEIN MAY PLAY A ROLE IN THE BIOSYNTHESIS OF THE PROSTHETIC GROUP OF NITROGERASE (FEMO COFACTOR).
28;
                                                                                                                                                                                                                                                                                                                                                                                   NIFE OR WTH1565.
Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NITROGENASE IRON-MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN NIFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70; DB 1; Length 478; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxidored_nitrognse_l.
Pfam. PF00148; Oxidored_nitro; 1.
PROSITE; PS00699; NITROGENASE_l_1; 1.
PROSITE; PS00699; NITROGENASE_l_1; 1.
Nitrogen fixation; Complete proteome.
Nitrogen 478 AA; 52909 MW; AE0285E766E46BFE CRC64;
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                                                                                                                                                                                                                                                                       478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: FE-MO COFACTOR BIOSYNTHESIS.
                                                                                                                                                                                                                                                                         PRT;
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MEDLINE-98037514; PubMed-9371463;
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                                                                                                                                                              271 RKAAYPAVSTFEKHSSSG 288
                                                                                                                                        129 KRALRAALNLLECGVSRG 146
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=145262;
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O27607;
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TISSUE-SPLEEN;
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088593
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(without alignments)
1129.948 Million cell updates/sec
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Q9gkl2 camelus dro
Q75594 homo sapien
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bombyx mori
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09v3b7
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09vv97
09vxx7
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097369
Q9b111
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                  Compugen Ltd
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GenCore version
Copyright (c) 1993 - 2000
                                                                                             December 17, 2001, 07:48:37
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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Q9XTN0
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O75594
Q9V4X2
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09HD75
09VV97
09VYX7
076537
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097369
Q9BLL1
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_human:*
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sp_unclassified:*
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sp_phage:*
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seq length: 200000000
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sp_virus:*
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Match Length
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Maximum DB
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TOWN-1998 (TEMBLE-1 08, Created)

TOWN-1998 (TEMBLE-1 17, Last annotation update)

TOWN-1998 (TEMBLE-1 17, Last annotation update)

TOWN-1998 (TEMBLE-1 17, Last annotation update)

BETTIONGLYCAN RECCGNITION PROTEIN PRECURSOR.

NOLINH-2001 (TEMBLE-1 17, Last annotation update)

EPETIONGLYCAN RECCGNITION PROTEIN PRECURSOR.

NOLINH-2004 (TEMBLE-1 17, Last annotation update)

EMBLIAND-10090;

NOSILTAXID-10090;

NOSILTAX
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kochwa H., Steubli F., Wasisi C., King B., Kochwa H., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Caninci P., de Bonaldo M.F., RA Gustinotch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustinotch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchioni L., Mashima J., Manbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., R. Hayashazaki Y., Punctional annotation of a full-length mouse cDNA collection."; N. K.
                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED FORMS.

-!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SPLEEN AND LUNG. ALSO DETECTED IN BRAIN AND THYMUS. IN THE LUNG, EXPRESSED IN THE PURKINUE CELLS OF THE CEREBELLUM AND IN THE BRAIN, EXPRESSED IN THE PURKINUE CELLS OF THE CEREBELLUM AND IN CETAIN LAYERS OF NEURONS IN THE HIPPOCAMPUS, ALSO DETECTED IN CELLS FILLING THE SPACE WITHIN THE INTESTINAL VILLUS.

-!- SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NFMDRVPAKRALRAALNILECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EQOARNVOHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMG 120
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                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                         INNATE IMMUNITY.
-1- FUNCTION: THE SOLUBLE FORM TRIGGERS APOPTOSIS IN VITRO.
-1- SUBCELLULAR LOCATION: EXISTS IN BOTH SOLUBLE AND MEMBRANE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 182; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
9844E2137F047F14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, APO16482, AAC31821.1; --
EMBL, AF005482, AAF06535.1; --
EMBL, AF008335, BAB25611.1; --
EMBL, AK008335, AAH05582.1; --
EMBL, X86374, CAA60133.1; ALT_SEQ.
EMBL, X12088; CAA72803.1; ALT_SEQ.
MGD, MGI:1345092; P91yrp.
MGD, MGI:1345092; P91yrp.
Immune response; Cytothee, Apoptosis; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AA; 20489 MW;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Strausberg R.;
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DISULFID
SEQUENCE
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1 MLFACALLALLGLAT-----SCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFC 54
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                                                                                                  Bukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Camelus dromedarius (Dromedary) (Arabian Camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameluse; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                1 MLFACA-LLALLGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDS
                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDOGLYCAN RECOGNITION PROTEIN. B6A1BD818030A7CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kappeler S.R., Farah Z., Puhan Z.; "Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan
                                                                                                                                                                                                                                                                                                                       ; Score 838.5; DB 11; Length 183; ; Pred. No. 2.8e-79; 10; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 70.6%; Pred. No. 3.2e-66;
Matches 132; Conservative 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recognition Protein.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131676; CAC19553.1;
                                                                                                                                                                                                                   Rehman A., Teodecki E.E., Krueger J.M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154114; AAF73252.1; - SB9C1B7AA8A2EC21 CRC64;
SEQUENCE 183 AA; 20590 WW; 5B9C1B7AA8A2EC21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-WAR-2001 (TrEMBLrel. 16, Last annotation update) PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PEPTIDOGLYCAN RECOGNITION PROTEIN PGRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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TISSUE-LACTATING MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 PC
193 PE
21377 MW;
                                                                                                                                                                                                                                                                                                                              Ouery Match 84.2%;
Best Local Similarity 84.7%;
Matches 155; Conservative 1
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                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YRE 183
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SEQUENCE
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PRELIMINARY;

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Matches
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TISSUE-BONE MARROW;
MEDLINE-98374308; PubMed-9707603;
Kang D., Liu G., Lundstroom A., Gelius E., Steiner H.;

R peptidoglycan recognition protein in innate immunity conserved from insects to humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN AND IS INVOLVED IN
                                   NSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSI 114
                                                            GITFMGNFMDRVPAKRALRAALNILLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVI 174
                                                                                                                                                                                  SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Richardson P., Sakaldasis G.,

Lamerdin J.E., McCready P.M., Scott D., Johnson G., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Scott D., Johnson G., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,

Erler A., Christensen M., Georgescu A., Avila J., Attix C.,

Andreise T., Anico-Keller G., Coefield J., Duarte S., Lucas S.,

Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C

Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: EXISTS IN BOTH SOLUBLE AND MEMBRANE-ASSOCIATED FORMS (BY SIMILARITY).
TIGSUE SPECIFICITY: HIGHLY EXPRESSED IN BONE MARROW. WEAK EXPRESSION FOUND IN KIDNEY, LIVER, SMALL INTESTIRE, SPLEEN, THYMUS, PERIPHERAL LEUKOCYTE, LUNG AND FETAL SPLEEN.
SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PŌTENTIAL.
PEPTIDOGLYCAN RECOGNITION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE SOLUBLE FORM TRIGGERS APOPTOSIS IN VITRO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D954C51440DC27DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 95:10078-10082(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AA; 21731 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  175 QSWEHYR 181
                                                                                                                                                                                                                                                                                                                                               186 QTWSHYR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00806; 1 MIM; 604963; -.
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RA MEDLINE-201960(6); PubMed-1073112;
RA Adams M.D., Celniker S.E., Li P.W. Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W. Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Feififer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Feififer B.D.,
RA Ballew R.M., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayterktaroglu L., Basaley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Bulter H., Cadlew E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Bulter H., Cadlew E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Bulter H., Cadlew E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Bulter R.M., Dayan-Rocha S., Dunkov B.C., Dun R.A.
Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun R.A.
Burtis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Well M.H., I. Degwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Waltel B., McIntosh T.C., McIrat S., Mount S.M., Malshum N.V., Mobrary D.M., Northes J., Moster B., Spatel I., Lay M., Norn M., Norn S., Norlis J., Moster B., Spatel F., Spatel M., Strong R., Shu E.,
Reinert K., Remington K.A., Shunders R.D.C., Scheeler F., Shen H.,
Ray Mang Z.-Y., Wassarman D.A., Weinston M., Strong R., Shu E.,
Ray Shies E., Spatel T., Woodage T., Worley C., Wu D., Yang S., Zho C., Zhapleng G., Zhan R., Zhong Y., Yang S., Zhon S., Zhon S., Zhon S., Zhon S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                       53 FCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPM 112
                                                                                                                                                                                   SIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ 172
                                                                                                                                                                                                                                                                  Gaps
                                                                        1 MLFACALLALLGLATS-----CSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGS
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Pred. No. 5e-64;
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Last annotation update)
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                                       21;
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                     127; Conservative
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186 LIONWPHYR 194
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                     Local
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Q9V4X2
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Query Match 38.0%
Best Local Similarity 40.5%
Matches 75; Conservative
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                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE 36
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GG8577 PROTEIN AND CG14746 PROTEIN (PEPTIDOGLYCAN-RECOGNITION PROTEIN-
                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                     61 EQQARNYQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMG 120
                                                                                                                                              121 NFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHY 180
                                                                                                                                                                               123 NYNTNTLTSAQITAAKGLLSDAVSRGQIVSGYILYGHRQVGSTECPGTNIWNEIRTWSNW 182
                                                                                                      1 MLFACALLALLGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSC 60
                                                                                                                Gaps
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8
                                                                        Length 184;
                                                                        38.6%; Score 384; DB 5; Length 18
42.5%; Pred. No. 4.4e-32;
Live 33; Mismatches 63; Indels
                                                  0F99D04914B07238 CRC64;
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Bent, Ae003836; AAF59051.1; -.
HSSP; P00806; LARO.
FlyBase: FBggn0033328; CG14745.
SEQUENCE 184 AA; 19829 WW; 0F99D04914B07238 CRC
                                                                                                                                                                                                                                                                                         Last sequence update)
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                                                                                          33; Mismatches
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                                                                                           Conservative
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                                                                            Query Match
Best Local Similarity
Matches 77; Conserva
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Q9V3B7
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Wassanman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RI "The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20558582; PubMed-11106397; WEDLINE-20558582; PubMed-11106397; Werner T., Liu G., Kang D., Ekengren S., Steiner H., Hultmark D., "A family of peptidoglycan recognition proteins in the fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 38.3%; Score 381; DB 5; Length 185; Best Local Similarity 41.7%; Pred. No. 9.1e-32; Matches 75; Conservative 30; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Indels
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Zhang W., Wan T., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARF94518; ARF95599.1; -
InterPro; IFR002086; Aldehyde_dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
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368 AA; 40020 MW; 1E74970732A5DAFD CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 40.0 KDA PROTEIN.
HOMO sapiens (Human).
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Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000)

Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000)

EMBL; ARD03836; ARF59054.1;

EMBL; AF207542; AAG23736.1; -.
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40:5%; Pred. No. 4.4e-31;
Live 33; Mismatches 61;
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FlyBase; FBGN0033325; CG14746.
FlyBase; FBGN0033327; PGRP-SC1
SEQUENCE 185 AA; 20395 MW;
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RAMAN-BURELEY;
RAMAN-PURELEY;
RAMAND CELNIKAR S.E., Holated;
RAMAND COROGORY R.A. Levis S.E., Informed S.., Amburner M., Henderson S.N.,
RAMAND R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RAMAND R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RAMAND R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RAMAND R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RAMAND R.M., Basu M., Baxendale J., Rayraktaroglu L., Beasley E.M.,
RAMAND R.C., Bouck J., Byraktaroglu L., Beasley E.M.,
RAMAND R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RAMAND R.M., Cavley S., Danike C., Davenport L. B., Davisko P.,
RAMAND R.M., Cavley S., Danike C., Davenport L. B., Davisko P.,
RAMAND R.M., Cavley S., Danike C., Davenport L. B., Daviss P.,
RAMAND R.J., Evangelista C.C., Ferraz C., Ferrara S., Fleischmann W.,
RAMAND R.J., Brougelista C.C., Ferraz C., Ferrara S., Fleischmann W.,
RAMAND R.M., Houston K.A., Howlann T.J., Hernandez J.R., Rock M., Laisaser K.A.,
RAMAND R.M., Laish R.M., McIncoon R.C., Marish D.M., Nelson D.L.,
RAMAND R.M., McIncoon T.C., McIedo M.P., McIncoon D.K.,
Ramalson D.R., Melson K.A., Nixon K., Nuxany D.M., Websel D.C.,
RAMAND R.M., McIncoon M., Stupski M.P., Sain H.,
Rabiazzolo M., McIncoon M., Suuders R.D.C., Scheeler F., Shen H.,
Rabiazzolo M., Pittanos I.J., Simpson M., Stupski M.P., Shu B.C., Stand R.M.,
Rabias R.M., Mcodage T., Worly K.C., Wu D., Yang S.
                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                              117 TEMGNEMDRVPAKRALRAALNILECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQS 176
                                                                                                                                               10 LLGLATSCSFIVPRSEWR-----AL-----PSECSSRLGHPVRYVVISHTAGSFCNS
                                                                       57 PDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGI
                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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REDINE-20196006; PubMed-10731132;

RA Adams M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Foskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandaell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Bacter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Bladwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Cawles P.F., Bhannari D., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler G., Davenport L.B., Davies P.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garrell J.H., Gu Z., Gunn P., Harris N.L.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Lasko P., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Mulshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Mallshina N.V., Mobarry C., Morris J., Puri V., Rah Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.
RA Spier E., Spradling A.C., Stabelchom M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinston B.H., Wang X., Wang X., Wang X., Wang Z.-Y., Wassarman D.A., Weinstone R.M., Wang X., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 QARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ACALLALIGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAG-SFCNSPDSCEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0501709 PROTEIN (PEPTIDOGLYCAN-RECOGNITION PROTEIN-SA).
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Science 287:2185-2195(2000).
EMBL; AE003526; AAF4920.1. -
FlyBase; FBGN033658; CG9681.
SEQUENCE 190 AA; 20997 MW; A2F81E4903E8173E CRC64;
                                                                                                                                                                                                                                                                                                                                                          37.4%; Score 373; DB 5; 38.9%; Pred. No. 6.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 38.9
nes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches
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-!- FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN AND TRIGGERS THE
PROPENOLOXIDASE CASCADE WHICH IS AN IMPORTANT INSECT INNATE IMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LARVA;
MEDLINE-983743108; PubMed-9707603;
KRDIR D., Liu G., Lundstroem A., Gelius E., Steiner H.;
Ang D., Liu G., Lundstroem A., Gelius E., Steiner H.;
A peptidoglycan recognition protein in innate immunity conserved from
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu X., Smith H.O., Glubs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 NSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : :|:|| ||:||| ||:||| ||:||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichoplusia ni (Cabbage looper).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Lepidoptera; Glossata; Ditrysia;
Moctuoidea: Noctuidae; Plusiinae; Trichoplusia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLALLGLATS-----CSFIVPRSEWRALPSECSSRLG-----HPVRYVVISHTAGSFC 54
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-1- INDUCTION: BY BACTERIAL CHALLENGE.
-1- SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LLAFVSAGKSRORSPANCPTIKLKROWGGKPS----LGLHYQVRPIRYVVIHHTVTGEC
                                                                                                                                                                                                                                                                                    STRAIN-DP CL CN BW;
MEDLINE-20558582; PubMed-11106397;
Werner T., Liu G., Kang D., Ekengren S., Steiner H., Hultmark D.;
Wa family of peptidoglycan recognition proteins in the fruit fly
Drosophila melanogaster.;
Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FBGn0030310; PGRP-SA.
203 AA; 22260 MW; D200A6EA79C66731 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.5%; Score 364; DB 5;
42.5%; Pred. No. 6e-30;
tive 27; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AA
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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SUBUNIT: MONOMER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF207540; AAG23734.1; -
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AF207541; AAG23735.1;
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Best Local Similarity 42.55
Matches 79; Conservative
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase;
SEOUENCE
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79 DVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFWDRVPAKRALRAALNL 138
                                                                                                                                                                                                                                                          80 IGSSFIIGGNGKVYEGAGMLHVGAHTYG-YNRKSIGITFIGNYNNDKPTQKSLDALRALL 138
                                                                                                                                                                                                                                         80 VAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMDRVPAKRALRAALNLL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 IVPRSEWRALPSECSSRLGHPVRYVVISHTA-GSFCNSPDSCEQQARNVQHYHKNELGWC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 20 IVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHKNELGWCD 79
                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx
                                                                                                                                                       Gaps
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ش
                                        PEPTIDOGLYCAN RECOGNITION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%; Score 335.5; DB 5; Length 208; 40.7%; Pred. No. 5.6e-27; Live 27; Mismatches 66; Indels 3
                                                                                                                         36.4%; Score 362.5; DB 5; Length 182; 44.1%; Pred. No. 7.5e-30; Live 26; Mismatches 63; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang J., Taniai K., Yamakawa M.;
"Bacteriophage T7 lysozyme-like protein l (BTL-LP1) cDNA.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB017519; BAB332941.;
SEQUENCE 208 AA; 23117 MW; DF02FB621AC9AD16 CRC64;
                                                                     POTENTIAL.
56631E762AE34794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 LECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BACTERIOPHAGE T7 LYSOZYME-LIKE PROTEIN 1 (BTL-LP1).
                                                                                                                                                                                                                                                                                                                   140 ECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHY 180
                                                                                                                                                                                                                                                                                                                                                                                                           208 AA
                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                     60 Po
20572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 13, C) (TrEMBLrel. 13, I) (TrEMBLrel. 17, I
EMBL; AF076481; AAC31820.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Conservative
                                                                                                                                                          71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombyx mori (Silk moth)
               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                            Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7091;
                   Immune response;
                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BLL2;
01-JUN-2001
                                                         DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09VXN9;
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                               SIGNAL
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ID 099
AC 099
DT 011
DT 011
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.. M 130 RALRAALNILECGVSRGFLRSNYEVKGHRDVOSTLSPGDQLYQVIQSWEHY 180

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RA MEDILANE ZULYOUOUS; FUDNECTION JAMES AND CAGAYNE J.D.,
RA AMANATICE Z.D. FULL RAY,
RA AMANATICE Z.D. CELLIKE S.D., SABBURNER M., GELIA R.P.,
AMANATICE G.C., SCHORTER S.E., RICHARGS S., ASABURNER M., PETGIFFER B.D.,
RA SULTON G.G., WORTHAN J.R., ZANAGO G., Chen L.X.,
AND STATE OF G., SARGET Y.H.C., Blazef R.G., Champpe M., PETGIFFER B.D.,
RA BAILOW R.H., DOYLE C., BAXTER E.G., FIBLE G., Champpe M., PETGIFFER B.D.,
RA ADAIL J.F., ABOYDE C., BAYEN STEACH C.R., MIXIOS G.L.G.,
RA ADAIL J.F., ABOYDE C., BAYEN STEACH D., BOLSHAKOY S.,
RA BAILOW R.H., BOSU A., AN H.-J., ANDTWAST PETACK C. BLANDAR D.,
BALTIS K.C., BUSAM D.A., BUNKL M., BOLCHAM M.R., BOUCK M., BOCCHAM M.R., BOUCK M., CAWLEY S.,
BUTLIS K.C., BUSAM D.A., DANINE C., DAVARSTEIN D., BOLSHAKOY S.,
RA BOTKOWA D., BOLCHAM M.R., BOUCK J., BROXEVEIN D., BOLCHAR A.,
BUTLIS K.C., BUSAM D.A., DANINE C., DAVARDOTT L.B., DAVIES P.,
RA CHETTY J.M., CAWLEY S., DANINE C., DAVARDOTT L.B., DAVIES P.,
RA DULPIN K.J., FANAGORISTA C., PETTAZ C., FETTAZ C., PETTAZ C.,
RA DULPIN K.J., EVANGELISTA C.C., FETTAZ C., FETTAZ C., MAYS A.D., DEW I., DIGLE S.M.,
RA DULPIN K.J., EVANGELISTA C.C., FETTAZ C., FETTAZ C., RETISCHMANIN M.,
RA HATTIS N.L., HARVEY D., HEIMAN T.J., WEI M.-H., IDEGWAM C.,
RA JALAID M., KALUSH F., KATPON G.H., RAY, MET M.-H., IDEGWAM C.,
RA JALAID M., KALUSH F., KATPON G.H., REZ., KENDISON J., MONTHY S., MONTHY S., WONDARTY C., MONTHIS M., MONTHON M., MUTCHON M., SLURS K.P., MOPPHERSON D.,
RA LOSK P. Leit Y. LEVITSKY A.N., LI J., WEIN M., PRESE M. G.,
RA LOSK P., LEIT Y., LEVITSKY A.N., LI J., WENDER S., WOLL S., WONDARTY C., MOLTIS J., WOSPHEET S., SANAGOR S.,
RA LOSK P., LEIT W., PULT W., WODDATTY C., MOLTIS J., WOSPHEET S., SANAGOR S.,
RA RELIGHT S.M., WORDANG T.C., SCHEELE F., SPARL T.,
RAIL M., MASSARMAND S., WOLLES E., WORDANG T., WOLL S., WORD S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOLL S., WOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFIVPRSEWRA-LPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQA-----RNVQHY 70
                  PGRP-LE OR CG8995.

Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;

Eukaryota, Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20558582; PubMed-11106397;
Werner T., Liu G., Kang D., Ekengren S., Steiner H., Hultmark D.;
"A family of peptidoglycan recognition proteins in the fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 334; DB 5; Length 345; 43.9%; Pred. No. 1.5e-26; tive 27; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBGn0030695; PGRP-LE.
SEQUENCE 345 AA; 39426 MW; 66CC484B54705AD7 CRC64;
CG8995 PROTEIN (PEPTIDOGLYCAN-RECOGNITION PROTEIN-LE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.";
Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000)
EMBL; AE003500; AAF48519.1; -.
                                                                                                                                                                                                    STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 75; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
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RAM MEDLINE—201960006; PubMed=10/2112;

RA Adams M.D. Celliker S.E., Il P.M., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celliker S.E., Il P.M., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Baxter E.G., Halt G., Champhe M., Pfelifer B.D.,

RA Brandon R.C., Baxter E.G., Halt G., Nalson C.R., Miklos G.L.G.

RA Barlew R.M., Baxdendale J., Bayraktarcglu L. Basaley E.M.,

RA Ballew R.M., Baxdendale J., Bayraktarcglu L. Beasley E.M.,

RA Ballew R.M., Baxdendale J., Bayraktarcglu L. Beasley E.M.,

RA Borkova D., Botchan M.R., Bouck J., Brokatin P., Brotchan M.R., Bouck J., Brokatin D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokatin P., Brotchan M.R., Bouck J., Brokatin D., Dew I., Dietz S.M.,

RA Borkova D., Botchan M.R., Bouck J., Brokatin P., Brotler P.,

RA Dorbins M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbins M., Dengelista C.C., Ferraz C., Ferraz C., Perrias C., Dunn P.,

RA Durbin K.J., Bavagelista C.C., Ferraz C., Ferraz C., Perraz C., Gabriellan A.E., Gary N.S., Galbart W.M., Glasser K.,

RA Durbin K.J., Bavay D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Well M.H., Ibeywam C.,

RA Astlush F., Karpen G.H., Kez Y., Karpen G.H., Kez Y., Kanther S., Kulp D., Lal Z.,

R. Lisko P., Lei Y., Levittsky A.A., Li J., Li Z., Lidna Y., Lin X.,

R. Lisko P., Lei Y., Levittsky A.A., Li J., Li Z., Lidna Y., Welson D.L.,

Mount S.M., Woyl M., Wurphy B., Wurphy L., Muzny D.M., Nelson D.L.,

RA Mang S.M., Nelson K.A., Whorley R., Worley K., Wu D., Yang S., Yao Q.A.,

RA Beinert K., Remington K.A., Wurder E., Wang A.H., Wang X.,

RA Beinert K., Remington K.A., Wurley R.C., Wu D., Yang S., Zhon W., Shinth H.O.,

RA Sher E., Sprading A., Stone R., Shon M., Stene B., Stone R., Shon F., Shon F., Rabong F., Worley K.C., Wu D., Yang S., Zhu X., Shilth H., Shin R., Rolson C., Stableter R., Spradez B., Shon F., Shon F., Radong R., Rad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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FBGD0035977; CG4437.
337 AA; 38180 MW; COACOBC955226C2E CRC64;
                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                   337
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                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
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EMBL; AE003552; AAF50301.1)
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                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Dros
NCBI_TaxID=7227;
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01-JUN-2000 (TrE
CG4437 PROTEIN.
CG4437.
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Best Local Simi
Matches 60;
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SEQUENCE
                                                                                                                                                                                                                                                                   09VSW0;
                                                                                                                                                                                                                           09VSW0
                                                                                                                                                    13
                                                                                                                                                        RESULT
                                                                                                                                                                                         09VSW0
                                                                                                                                                                                                                              SO DRY READ BY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οχ
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Best Local Similarity
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                                                                                                                                      19
                    Matches
                                                                                                                                                                                                                                                                                                                                             96VV60
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                         WCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMDRVPAKRALRAAL 136
                                                              85 WVDIGYNFLYGGDGQIYVGRGWHIOGQHVNG-YGAISVSIAFIGTFVNMEPPARQIEAK 143
    27 ILDRSEWLGEPP--SGKYPHLKLPVSNIIIHHTATEGCEQEDVCIYRMKTIQAFHMKSFG
                                                                                                                       137 NELECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYRE 182
                                                                                                                                                09B0C5A7CF4BBF85 CRC64;
                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                  186 AA
                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000)
EMBL; AE003558; AAF50530.1;
                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0035806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                      CG7496 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; 1
SEQUENCE
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Length 186;

DB 5;

32.3%; Score 322;

Query Match

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RESTRAIN-BERKELEY.

RAMAIN-BERKELEY.

RAMAIN-BERKELEY.

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Brosophila Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Brkaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                     DVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMDRVPAKRALRAALNL 138
                                                                                                                                                                              Gaps
                                                                  20 IVPRSEWRAL-PSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHKNELGWC 78
                                                                                              22 IVTRAEWNAKPPNGAIDSMETPLPRAVIAHTAGGACADDVTCSQHWQNEQNEQMSKQKFS
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                                 Indels
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                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
           Pred. No. 1.2e-25;
); Mismatches 64;
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41.5%; Fic. 30;
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                                   Conservative
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                                                   Query Match 32.3%; Score 321.5; DB 5; Length 182; Best Local Similarity 39.4%; Pred. No. 1.3e-25; Matches 69; Conservative 29; Mismatches 74; Indels 3
Flybase; FBgn0036657; CG9697.
SEQUENCE 182 AA; 20459 MW; 99AC18AD426BC308 CRC64;
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Search completed: December 17, 2001, 07:50:01 Job time: 84 sec

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December 17, 2001, 07:48:37; Search time 23.37 Seconds (without alignments) 576.865 Million cell updates/sec
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1 MLFACALLALLGLATSCSFI.....TLSPGDQLYQVIQSWEHYRE 182
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522463 seqs, 74073290 residues
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Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result 80

Murhe granulocyte Human tag7 clone p Human PRO1269 prot Htag7 protein enco Chondrosarcoma pep Human PRO1269 (UNO Protein of the inv Bovine granulocyte Mouse taq7 clone p Human full length Human full length Description AAY96964 AAY99400 AAB66149 AAW23722 AAE00693 AAY00770 AAB24022 ΩÏ DB Query Match Length 100.0 Score

Wound healing tiss Amino acid sequenc Amino acid sequenc Recombinant peptid Amino acid sequenc Human protein clon Keratinocyte pepti	Human secreted pro Murine peptidoglyc Human 5' EST relat C glutamicum prote Human Zgpal domain	peptidoglyc tag7 clone AFP protein truncated g de #10335 en	0000 61	Arg-gingipain high Arg-gingipain-2 am Porphyromonas ging P. gingivalis haem Haemagglutinin pro Arg-gingipain-2 pr Arg-gingipain-2 pr Arg-gingipain-2 pr Arg-gingipain-2 pr Arg-gingipain-2 am PrtR antigenic pro Human protein segu
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21 19 19 21 21 21	22222	55 55 55 55 55 55 55 55 55 55 55 55 55	10 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	22 22 23 23 23 23 23
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ALIGNMENTS

Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; mouse. Prokhorchouk E; Georgiev G, Kiselev S, Ostermann E, (BOEH) BOEHRINGER INGELHEIM INT GMBH. AAY00770 standard; Protein; 182 AA. Mouse tag7 clone protein sequence. 98WO-EP04287 97US-0893764 (first entry) WO9902686-A1. 10-JUL-1998; 11-JUL-1997; 18-MAY-1999 21-JAN-1999. AAY00770; Mus sp. AAY00770 RESULT

New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and leukaemia

WPI; 1999-120887/10. N-PSDB; AAX21819.

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18-MAY-1999
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                 This sequence is the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarroma (Raposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antiagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                                                                                                                                                                                                                                                                      61 EQQARNVQHYHKNELGWCDVAXNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMG 120
                                                                                                                                                                                                                                                                                                   NFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHY 180
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                                                                                                                                                                                Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine granulocyte peptide A precursor (antimicrobial MGP-A)
                                                                                                                                                                                                    Indels
                                                                                                                                                                                Score 996; DB 20;
Pred. No. 1.1e-99;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            AAW23723 standard; Protein; 181 AA
  Claim 19; Fig 1; 138pp; English.
                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 182; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endotoxaemia; mouse
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This protein comprises the precursor of a novel, claimed antimicrobial peptide from murine neutrophils, designated murine artimicrobial peptide from murine neutrophils, designated murine cognitive peptide A or MGP-A (see AAM27372). Its anno acid sequence was deduced from a cDNA clone (see AAM78510) obtained from murine bone marrow. MGP-A and the bovine homologue, BGP-A (see AAW23724), exhibit activity against Gram-positive and Gram-negative bacteria, fungi and viruses, specifically staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary in properticularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post harvest spoilage or expressed in transgenic plants to increase their disease. They have low immunogenicity. Carboxamidated analogues of MGP-A and BGP-A may also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVLQSWEHY 180
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melanoma; leukaemia; apoptosis inducer; human.
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                                                                               Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
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97.8%; Pred. No. 1.6e-95;
.ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                        Claim 9; Fig 5; 56pp; English
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WPI; 1997-424753/39.
N-PSDB; AAT78510.
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                                                                                                                                                                 This sequence is the human tag? of the invention. Cells containing the tag? DNA sequence are used to express recombinant tag? Tag? Is used to produce and purify antibodies; to inhibit growth of mammallan tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Raposi's,
                                                                                                                                                                                                                                                         induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 SIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                           osteo or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induce apoptosis. The tag7 coding sequences are also useful as probes for ge
                                                                                                                                                                                                                                                                                                                                                                                                                             MLFACALLALLGLATS-----CSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mllawalps11r1gaaqetedpaccspivprnewkalasecaqhls1p1ryvvvshtags 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumourigenesis; anticancer; detection.
                                                                                                       induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
                                                                                              New nucleic acid encoding tag7 . used to inhibit tumour growth and
                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                             Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                    Ξ,
                                    Prokhorchouk
                                                                                                                                                                                                                                                                                                                                                                             69.5%; Score 692; DB 20; 67.2%; Pred. No. 8.5e-67; iive 21; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO1269 protein sequence SEQ ID NO:7.
                                                                                                                                           Claim 23; Page 126-127; 138pp; English
                                    Ostermann E,
            (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB24022 standard; Protein; 196 AA.
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.2%
Matches 127; Conservative
                                    Seorgiev G, Kiselev S,
                                                           WPI; 1999-120887/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 liqnwphyr 189
                                                                                                                                                                                                                                                                                                                                           191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 VIOSWEHYR 181
                                                                      N-PSDB; AAX21820
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                                                                                                                                                                                                                                                                                                                  metastasis.
                                                                                                                       leukaemia
                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonuclectide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AACS8019 to AACS8102 represent PCR primers and hybridisation sequences. AACS8103 to AACS8122 and AAB24021 to AAB24040 represent human PRO polynuclactide and protein sequences given in the exemplification of the present invention for human PRO polynuclactide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                          Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -53 FCNSPDSCEQOARNVQHYHKNELGWCDVAYNPLIGEDGHVYEGRGWNIKGDHTGPIWNPM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ 172
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                                                                                                                                                                                                                                 Wood WI;
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                                                                                                                                                                                                                                 Watanabe CK,
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67.2%; Pred. No. 8.8e-67;
ive 21; Mismatches 33;
                                                                                                                                                                                                                                    Roy MA,
                                                                                                                                                                                                                                    Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 61; Fig 4; 226pp; English.
                        99WO-US20111.
99US-0162506.
99WO-US28313.
99WO-US28634.
99WO-US05028
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                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                           WPI; 2000-594320/56.
N-PSDB; AAC58104.
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186 lignwphyr 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 VIQSWEHYR 181
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01-DEC-1999;
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08-MAR-1999;
01-SEP-1999;
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173 VIQSWEHYR 181 :||:| ||| 186 lignwphyr 194

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<u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #8 and protein sequences are represented in sequences AAA806613 and AAB2583. Sequences AAA80662-A80663 represent genes related to the secreted protein gene#8.
          Immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AABG066-880623 encode the 12 secreted protein sequences given in AABC576-B2559. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; antiparanty; antiarthritic; antirhamatic, antiproliferative, antiarthritic; antirhamatic, antiborderial; and antifungal activity. The proteins, antiviral; and antiangonists and be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPM 112
                                                                                                                                                                                                                                                                                                                                                                                 Wei Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 mllawalpsllrigaagetedpaccspivprnewkalasecaghlslplryvvvshtags 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLFACALLALLGLATS-------CSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated nucleic acid molecules encoding human secreted proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                 Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.5%; Score 692; DB 21; Length 196; 67.2%; Pred. No. 8.8e-67; Live 21; Mismatches 33; Indels
antifungal;
                                                                                                                                                                                                                                                                                                                                                                                   Kenny JJ,
antibacterlal;
                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Olsen HS, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Figure 34; 803pp; English.
vulnerary; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vounds, and infectious diseases
                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                  98US-0105971.
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Best Local Similarity
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                                                                                                                                                                              WO200029435-A1.
                                                                                                                                                                                                                                                                                                  28-OCT-1998;
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Matches
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Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; regulator; chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins are useful for preventing, treating or ameliorating a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DNA and
                                                                                    Chondrosarcoma peptidoglycan recognition protein-like protein.
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/label= Antigenic_region
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/label= Antigenic_region
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'label= Antigenic_region
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/label= Mature_protein
34..117
                                                                                                                                             .nhibitor; protein co-ordinate data.
                                                                                                                                                                                         Location/Qualifiers
                    AAY96964 standard; Protein; 196 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 3; 191pp; English.
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                                                                 (first entry)
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/label= Ar
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/label= 4
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18-SEP-1998;
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15-SEP-1998,
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condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TNF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
                                                                                                                                                                                  113 SIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ 172
                                                                                                                                                                                                                                8; Gaps
                                                                                                                                                 1 MLFACALLALLGLATS------CSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGS 52
                                                                                                                                                                                                                                                                                                                                                                                               Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                           69.5%; Score 692; DB 21; Length 196; 67.2%; Pred. No. 8.8e-67; ive 21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                             Human PRO1269 (UNO639) amino acid sequence SEQ ID NO:216.
                                                                                                                                                                                                                                                                                                                        AAY99400 standard; Protein; 196 AA.
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98US-0098749.
98US-0098803.
98US-0098803.
98US-0098843.
98US-0099536.
98US-0099546.
98US-0099541.
98US-0099642.
98US-0099741.
98US-0099754.
98US-0099754.
98US-0099763.
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                                                                                                           Query Match 69.5%
Best Local Similarity 67.2%
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                            08-AUG-2000 (first entry)
                                                                pulmonary fibrosis.
                                                                                                                                                                                                                                                                      :||:| |||
186 liqnwphyr 194
                                                                                  196 AA;
                                                                                                                                                                                                                                                          173 VIQSWEHYR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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10-SEP-1998;
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173 VIQSWEHYR 181 :||:| ||| 186 lignwphyr 194

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New manmalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig 122; 773pp; English.
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                                                                                                                     980S-0106464.
980S-0106856.
98US-0106902.
98US-0106905.
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98US-0106932.
98US-0106934.
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                98US-0106178.
98US-0106248.
98US-0106384.
98US-0108500.
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98US-0108850.
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98US-0108801
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N-PSDB; AAA37082.
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Best Local Similarity
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18-NOV-1998
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PRA RABBARA RA
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Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
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Hillan KJ;
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Gurney AL, H
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                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.5%; Score 692; DB 22;
67.2%; Pred. No. 8.8e-67;
ive 21; Mismatches 33;
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                                                                                                                                                                                                                                                                                                                                                                                                  Baker KP, Botstein D, Desnoyers L, Gao W, Goddard A, Godowski PJ, Grir Pan J, Paoni NF, Roy MA, Smith V, Watanabe CK, Williams PM, Wood WI;
                                                                                                              Secreted; transmembrane; gene therapy
           AAB66149 standard; protein; 196 AA.
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99US-0144758.
99US-0145698.
99WG-US20111.
99US-0162506.
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99WO-US30095.
2000WO-US00219.
2000WO-US00376.
                                                                                     Protein of the invention #61
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127; Conservative
                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-071395/08.
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30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
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06-JAN-2000;
                                                            02-APR-2001
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                                     AAB66149;
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Matches 12
AAB66149
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       Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                        178..190
/label- Mat_peptide
/note- "BGP-A antimicrobial peptide (Claim 2)"
                                                                                                                                                                                                                    Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; bovine granulocyte peptide A; BGP-A; preservative; sepsis;
                                                                                                                                                                                                Bovine granulocyte peptide A precursor (antimicrobial BGP-A)
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /label- Sig_peptide
                                                                                                                              AAW23722 standard; Protein; 190 AA
                                                                                                                                                                                                                                                                                                                                              /label= Propeptide
178..190
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                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                        endotoxaemia; cattle
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N-PSDB; AAT78509.
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186 liqnwphyr 194
                                                   173 VIQSWEHYR 181
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/label- Mature_full_length_Zgpal_protein_#2
/note= "This region functions as an immunogenic epitope"
20.29
/label- Immunogenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Defliciency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome l.
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                                                                                                                                                                                                                                                                              QQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGN 121
                                                                                                                                                                                                                                                          122 FMDRVPAKRALRAALNILECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYR 181
                                                                                  Gaps
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                                                                                                                   4 ACALLALLGL -- ATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human full length granulocyte peptide homolog Zgpal protein #2.
                                                 Length 190;
                                                                                  Indels
                                               ; Score 676; DB 18;
; Pred. No. 4.5e-65;
19; Mismatches 36;
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/label= Immunogenic_epitope
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label Hydrophilic_region
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|abel= Domain_1
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                                                 67.9%;
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'label= Hy
                                                 Query Match 67.9
Best Local Similarity 68.3
Matches 123; Conservative
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AA;
190
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Sequence
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/label= Immunogenic_epitope

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chomolog, Zgpal protein. Zgpal gene is located on human chromosome 1.

Capal polypeptides are useful for producing antibodies which are useful

for detecting cancer. Zgpal polypeptides having anti-microbial activity

are useful for treating dental carries, periodontal disease, thrush,

detecting cancer. Zgpal polypeptides having anti-microbial activity are

useful for treating dental carries, periodontal disease, thrush,

castrointestinal disease, uninary tract infections, vaginal infections,

respiratory infections, acquired immune deficiency syndrome (ALDS) and

lung infections associated with cystic fibrosis and prevention of

cinfection in skin and other epithalial wounds. Zgpal-cytokine fusion

proteins are useful for enhancing in vivo killing of target tissues

(epithelial cancers, and more specifically lung, ovarian and rectal

cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are

useful in in vitro studies of exogenous microorganism infections such as

bacterial, viral or fungal infection and also to study epithelial cell

defensin induction in cell culture. Zgpal antibodies, polyuculectides and

anti-zgpal antibodies, thus serving as markers for detecting genetic

diseases or cancers. Zgpal sequences are useful as diagnostics in

canti-zgpal antibodies, thus serving as markers for detecting genetic

forensic DNA profiling and as probes or primers to clone 5' non-coding

cregions of a zgpal gene. Zgpal antibodies are useful for servening expression libraries and as

chat express zgpal, for screening expression libraries and as

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"This region is specifically claimed in claim 18"
                                                                                                                                                             /label= Immunogenic_epitope
/note= "This region is specifically claimed in claim 18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
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43.8%; Pred. No. 1.7e-35;
tive 33; Mismatches 60;
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/label= Immunogenic_epitope
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/label= Immunogenic_epitope
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                                                                        'label Domain_2
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12-JUL-2000; 2000US-0218070.
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N-PSDB; AAD04006.
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Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; ATDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome 1.
                                                                                                                                                                                                                                                                                                                              18.375
/label= Mature_full_length_2gpal_protein_#1
/note= "This region functions as an immunogenic epitope"
                                                                                                                                                                                                                                                                                                                                                                         /label= ImmunogeniC_epitope
/note= "This region is specifically claimed in claim 18"
              73 NELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFMGNFMDRVPAKRAL 132
                                                                                                                                                                              Human full length granulocyte peptide homolog Zgpal protein #1.
                                                      133 RAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYR
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| label = Hydrophilic_region
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'label= Hydrophilic_region
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'label= Hydrophilic_region
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'label= Hydrophilic_region
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                                                                                                                                                                                                                                                                                                                       'label= Signal_peptide
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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2000US-0218070
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N-PSDB; AAD04004.
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12-JUL-2000;
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                                                                                                                                       AAE00692;
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Peptide
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7..32 |abel= Antigenic_region

Region Region Domain Region
'label= Mature_protein

0..58 label= Antigenic_region 52..135 /label- PGRP-like_domain 2..99 label- Antigenic_region

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changing, 2gpal protein. 2gpal gene is located on human chromosome 1.

Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. 2gpal polypeptides having anti-inacrobial activity are useful for treating dental carries, periodontal disease, thrush, detecting cancer. 2gpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, vaginal infections, respiratory infections, acquired immune deficiency syndrome (AIDS) and line time associated with cystic fibrosis and prevention of infection in skin and other epithelial wounds. Zgpal-cytokine fusion proteins are useful for enhancing in vivo killing of target tissues cancers, and more specifically lung, ovarian and rectal cancers, and more specifically lung, ovarian and rectal cancers, and more specifically lung, ovarian and rectal cancers, ragments, fusion proteins or agonists are useful in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal infection and also to study epithelial cell defensin induction in cell culture. Zgpal antibodies, mann or americal cancers and effection and also to study epithelial cell defensin induction in cell culture. Zgpal antibodies, mann or americal cancers and anti-zgpal antibodies, thus serving as markers for detecting genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 drlkscdigynflvgqdgaiyegvgwnvqgsst-pgyddialgitfmgtftgippnaaal 325
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                                                                                                                                                            present sequence is human full length granulocyte peptide (GP-A)
New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
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43.8%; Pred. No. 1.7e-35;
Live 33; Mismatches 60;
                                                                                                         Claim 14; Page 105-106; 114pp; English
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Local Sim.
74;
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Matches 74
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/label= Antigenic_region 186..207 /label= Antigenic_region 214..225

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WO200039327-A1.

06-JUL-2000

(HUMA-) HUMAN GENOME SCI INC

98US-0113809.

23-DEC-1998;

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133 RAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYR 181
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Peptidoglycan recognition protein-like protein; PGRP; PGRP-W; regulator;
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                                                                         AAY96963 standard; Protein; 368
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1..17 /label= Signal_peptide 18..368 Location/Qualifiers

> Protein Peptide

4 Gaps 16; 38.0%; Score 378; DB 21; Length 368; 40.5%; Pred. No. 1.8e-32; ive 33; Mismatches 61; Indels 1 75; Conservative Query Match Best Local Similarity Matches 75; Conserv

Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-K), are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TMF) and TNF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal Olsen HS; Claim 11; Fig 2A-B; 191pp; English. Rosen CA, Ruben SM, Young PE, WPI; 2000-452414/39. N-PSDB; AAA51718. pulmonary fibrosis AA; Sequence

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60 CEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGITFM 119
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38.8%; Pred. No. 3.6e-27;
cive 29; Mismatches 80
                                                                                                                              AAW37835 standard; Protein; 196 AA
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N-PSDB; AAV19148.
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186 wle 188
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                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the silkworm peptidoglycan recognition protein.
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                      TFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQS 176
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       LLGLATSCSFIVPRSEWR----AL----PSECSSRLGHPVRYVVISHTAGSFCNS
                                                                     244 sdecrllvrdigsfyldrlkscdigynflvgqdgaiyegygwnyggsst-pgyddialgi
                                                       PDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPMSIGI
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N-PSDB; AAV19149.
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Recombinant peptidoglycan recognition protein - and genes coding for peptidoglycan recognition proteins
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AAW37834
ID AAW37834 standard; protein; 173 AA.
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20 IVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHKNELGWCD 79 31.5%; Score 313.5; DB 19; Length 173; 39.3%; Pred. No. 6e-26; Live 25; Mismatches 73; Indels 1; Best Local Similarity 39.33 Matches 64; Conservative Query Match õ g õ

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140 ECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQVIQSWEHYRE 182

Search completed: December 17, 2001, 07:49:31 Job time: 54 sec

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186002 i AC006933 Drosophila melan
280887 i AE003526 Drosophila melan
622 i AB017520 Bombyx mori mRNA fo
1803 i AE149837 Mus musculus TAGL-
107216 i AC010028 Drosophila melan
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Unclassified.
1 (bases 1 to 549)
2 (Georgiav.G.P., Kiselev.S.L., Prokhorchouk,E.B. and Ostermann,E. Nucleic acid encoding tag7 polypeptide
Patent: US 6172211-A 1 09-JAN-2001;
Location/Qualifiers
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gb_ro:AF149837
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AUTHORS
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1158 | AF207537 Drosophila melanogas
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-MODEL=frame+_p2n.model -DEV=xlp
-Q=Cqqn2_1\U74947_26111/app_query.fasta_1.241
-Q=Cqqn2_1\U7494PQ_spool/VG09462625/runat_17122001_074947_26111/app_query.fasta_1.241
-Q=Cqpq02_1\U74PPTO_spool/VG09462625/runat_17122001_074947_26111/app_query.fasta_1.241
-Q=Cqpq02_1\U74PPTO_spool/VG09462625/runat_17122001_0700 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-VGAPEXT=0.000 -VGAPEXT=0.050 -XGAPEXT=0.500
-FGAPOP=4.500 -FGAPEXT=7.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPEXT=0.000
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-NORM=ext -MINLEN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER-US09462625_eCGNI_1_0 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                       Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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     OM of: US-09-462-625-2
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9D_hig: AF076481

9D_li: AF007833

9D_li: AF07783

9D_li: AF07783
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WLFACALLALLCLATSCSFIVPRSEWRALPSECSSRLGHPVRYV
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                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 669)
Slayton, W.B., Rigaa, A., Hancock, J.D., Zaugg, J.K., Le, T.V.,
Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R.
Granulocyte-colony stimulating factor up-regulates expression of murine tag7 during myeloid differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Characteristics (699)

2. (bases I to 669)

2. (bases I to 669)

2. Sayton, W.B., Rajoac, A., Hancock, J.D., Zaugg, J.K., Le, T.V.,

Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R.

Direct Submission

Submitted (11-0CT-1999) Pediatrics, University of Utah, 50 North

Medical Drive, Room 22,126, Salt Lake City, UT 84132, USA

Location/Qualifiers
                                                                                                                                                                                             07-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 sSerPhelleValProArgSerGluTrpArgAlaLeuProSerGluCysS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 erSerArgLeuGlyHisProValArgTyrValValIleSerHisThrAla 50
                                                                                                                                                                                   AF193843 669 bp mRNA ROD
Mus musculus TAG7-like protein mRNA, complete cds.
AF193843
AF193843.1 GI:6273360
             151 ASnTyrGluValLySGlyHiSArgASpValGlnSerThrLeuSerProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 182
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 5.473 Percent Similarity: 100.000
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US-09-462-625-2 x AF193843
                                                                                                                                                                                seq_documentation_block:
LOCUS AF193843
                                                                                                                                            seq_name: gb_ro:AF193843
                                                                                                                                                                                                                                                                                          house mouse.
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1 (bases 1 to 680)

Rang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.
A peptidoglycan recognition protein in innate immunity conserved from insects to humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"peptidoglycan recognition protein precursor"/protein_id-"AAC31821.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H. Direct Submission
Direct Submission
Submitted (08-UIL-1998) Microbiology, Stockholm University, Stockholm S-106 91, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998)
98374308
                                                                                                                                                                                                                                                                                                      134 laalaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeuArgSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 heLeulleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIle 100
                                                                                                                                                                                                                            275 TCCTTATTGGAGGACGGTCATGTCTATGAAGGCCGAGGCTGGAACATC 324
                                                                                            67 lGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrAsnP

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    /db_xref="taxon:10090"

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AF076482
AF076482.1 GI:3342530
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LOCUS AF076482
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house mouse.
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AUTHORS
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KEYWORDS
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                   SOURCE
DHTGPIWNPMSIGITFWGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
QSTLSPGDQLYQVIQSWEHYRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS BC005582 713 bp mRNA ROD 12-JUL-2001
DEFINITION Mus musculus, peptidoglycan recognition protein, clone MGC:11430
ACCESSION BC005582 ACCESSION BC005582 GI:13542755
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84. .581
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1 216 c 174 g 144 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 TCCTTATTGGAGAGGACGTCATGTCTATGAAGGCCGAGGCTGGAACATC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 rPheMetGlyAsnPheMetAspArgValProAlaLySArgAlaLeuArgA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 CTTCATGGGGAACTTCATGGACCGGGTACCCGCAAAGCGGGCCCTCCGTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerProGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 GCAGCATTACCACAAGAATGAGCTGGGCTGGTGCGATGTAGCCTACAACT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 CAGTITCATCGTGCCCCGCAGTGAGTGGAGGCCCTGCCATCCGAGTGCT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 cragececeregecarceagreceraceregrearereacacacacaece 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 erSerArgLeuGlyHisProValArgTyrValValIleSerHisThrAla 50
                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                     36 ATGITGITTGCCTGTGCTCTCCTTGCCCTCGTGGGTCTGGCAACCTCCTG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 sSerPheIleValProArgSerGluTrpArgAlaLeuProSerGluCysS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 IGINHISTYTHISLYSASNGLULeuGlyTrpCysAspValAlaTyrAsnP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 yAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
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                                       36. .83
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US-09-462-625-2 x AF076482
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                                                                                                                                                                                                             alignment_scores
                                       sig_peptide
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ORIGIN
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: j Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3342530.
Location/Qualifiers
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DHTGPIWNPMSIGIIFWGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garcia,
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                   Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"peptidoglycan recognition protein"
/protein_id="AAH05582.1"
/db_xref-"GI:13542756"
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Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                            http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 713
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218 c 178 g
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                                                                                                                                                                                                                                                                               URL:
                                                                              1 (bases 1 to 713)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .595
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Percent Similarity: 100.000
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US-09-462-625-2 x BC005582
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                       BASE COUNT
                            gene
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                                                        CDS
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Kustikova,O.S., Kiselev,S.L., Borodulina,O.R., Senin,V.M., Afanas'eva,A.V. and Kabishev,A.A.
Cloning of the tag7 gene expressed in metastatic mouse tumors genetika 32 (5), 621-628 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiselev,S.L., Kustikova,O.S., Korobko,E.V., Prokhortchouk,E.B., Kabishev,A.A., Lukanidin,E.M. and Georgiev,G.P.
Molecular cloning and characterization of the mouse tag7 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-APR-1995) O.S. Kustikova, Inst of Gene Biology
Russian Academy, of Science, B334, Vavilov Street 34/5, Moscow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jul 6, 1995 this sequence version replaced gi:785010.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               546
                                                                                                                                                                                                                                    LysGlyAspHisThrGlyProlleTrpAsnProMetSerIleGlyIleTh 117
                                                                                                                                                                                                                                                                                              rPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLeuArgA 134
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296
                                                                                                                                                                            heLeulleGlyGluAspGlyHisValTyrGluGlyArgGlyTrpAsnIle 100
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                                                                                       197 GGCAGCTTCTGCAACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 TGACCAACTCTATCAGGTCATCCAAAGCTGGGAACACTACCGAGAG 592
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J. Biol. Chem. 273 (29), 18633-18639 (1998)
98325081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"/strain="A/Sn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.musculus mRNA for TAG7 protein.
X86374
X86374.1 GI:887524
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LOCUS MMRNATMc1
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JOURNAL
MEDLINE
REFERENCE
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TITLE
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                            134
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                                                           51
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a 216 c 173 g 143 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaArgAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 lGlnHisTyrHisLysAsnGluLeuGlyTrpCySAspValAlaTyrAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 rPheMetGlyAsnPheMetAspArg.ValProAlaLysArgAlaLeuArg
                                                                                                                                                                                                                                                                                                                                                         1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSerCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 183
Gaps: 2
Percent Identity: 97.814
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36. .491
                                                                                                                                                                                                                                                                                                                                   to: 678
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                                                                                       /codon_start=1
                              36. .491
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36. ^^01
                                                                            /gene="tag7"
                                                                                                                                                                                                                                                                                                                                       to: MMRNATMS1
                                                                                                                                                                                                                                                 950.50
5.310
97.814
                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-462-625-2 x MMRNATMS1
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369

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SNYEVKGHRDVQPILSPGDRLYFIIQTWSHYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus. I (Dases 1 to 700)

Kappeler, S. R., Farah, Z. and Puhan, Z.
Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-DEC-1998) Kappeler S.R., Institute of Food Science,
Swiss Federal Institute of Technology, LFO F25, 8092 Zurich,
SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDR131676 700 bp mRNA AAM 21-DEC-2000 Camelus dromedarius mRNA for peptidoglycan recognition protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="peptidoglycan recognition protein"
678. .683
247 c 201 g 122 t
                                                                                                                                                                                                                                                                               116 eThrPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaLeuA 133
                                                                                                                                                                                                                     SerAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSerPr 166
                                                                                                                                                                                                                                                                                                                                                                                       100 IleLysGlyAspHisThrGlyProIleTrpAsnProMetSerIleGlyIl 116
120 TGTGCAGCTTTACCAAATGAAACAGCTGGGCTGGTGCGATGTAGCCTACA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                166 oGlyAspGlnLeuTyrGlnValIleGlnSerTrpGluHisTyrArgGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sub_species="Somali breed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Camelus dromedarius"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ131676.1 GI:11990123
peptidoglycan recognition protein.
Arabian camel.
Camelus dromedarius
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_om:CDR131676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS CDR131676
DEFINITION Camelus drome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ131676
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mat_peptide
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JOURNAL
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=i
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                                                                                                                                                                                                                                                                                   Tobases 1 to 630)
Rehman, A., Teodecki, E.E. and Krueger, J.M.
Direct Submission
Submitted (25-MAY-1999) Veterinary Comparative Anatomy,
Pharmacology, and Physiology, Washington State University, P.O. Box 646520, Pullman, WA 99164, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Homo sapiens and Mus musculus
peptidoglycan recognition protein; similar to Trichoplusia
ni and Mus muşculus TAG7"
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                           AF154114 630 bp mRNA ROD 01-JUN-2000 Rattus norvegicus peptidoglycan recognition protein PGRP (Pgrp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nValGlnHisTyrHisLysAsnGluLeuGlyTrpCysAspValAlaTyrA 83
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Percent Identity: 84.699
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Sprague-Dawley/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="spleen
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 630
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                                                                                                                        AF154114.1 GI:8132325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Pgrp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dene="Pgrp"
                                                                                                     mRNA, complete cds.
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                                                                                                                                                                                 Norway rat.
Rattus norvegicus
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4.904
93.443
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US-09-462-625-2 x AF154114
                                        seq_documentation_block:
LOCUS AF154114
    seq_name: gb_ro:AF154114
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                                                                                DEFINITION
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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                           gene
               JOURNAL
                                                                                                                                                                                                                                        CDS
                                                                                                                           FEATURES
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A peptidoglycan recognition protein in innate immunity conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF076483 690 bp mRNA PRI 15-AUG-1998
Homo sapiens peptidoglycan recognition protein precursor (PGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 nSerThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnSerTrpG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMETSETILEGLYILEThrPheMetGlyAsnPheMetAspArgValProA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 laLysArgAlaLeuArgAlaAlaLeuAsnLeuLeuGluCysGlyValSer 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyArgGlyTrpAsnIleLysGlyAspHisThrGlyProIleTrpAsnPr 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 AGAAGACCCGCCGCCGCCTCCATCGTGCCCCCCCGAGAGTGGAGGG 139
                                                                                                                                                                                                                                                                                             289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 GGCCGAGGCTGGAACATCAAGGGCGCCCACGCAGGTCCCACCTGGAACCC 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAspValGl
                                                                                                                                                                                                                                                                       61 uGlnGlnAlaArgAsnValGlnHisTyrHisLysAsnGluLeuGlyTrpC
                                                                                                                                                                                                                                                                                                                                                                                                                         240 GCAGCAGGCCCAGAACGTGCAAAGCTACCATGTGCGGAACCTGGGCTGGT
                                                                                                                                              1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThr....
                                                                                                                                                                  40 GTGCTTCTCGTCTGGCCTCTCGCCTCGAGCGGAGCGGCTCG
                                                                                                                                                                                                           .....SerCysSerPhelleValProArgSerGluTrpArgA
                                                                                                                                                                                                                                                                                                                                       45 ValileSerHisThrAlaGlySerPheCysAsnSerProAspSerCysGl
                  Gaps: 1
Percent Identity: 70.588
 Length:
                                                                                                              to: 700
                                                                                                              from: 1
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                                                                                                              Align seg 1/1 to: CDR131676
713.00
4.456
85.561
                                                                              US-09-462-625-2 x CDR131676
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590 CACACTACCGC 600
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 Quality:
Ratio:
Percent Similarity:
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                                                                 alignment_block
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ECAQHLSLPLRYVVSHTAGSSCOMPASCQQARNYQHYHKKTLGWCDVGYRFLIGED
GLYYEGRGWNFTGAHSGHLWNPMSIGISFWGWYMYDRVPTPQAIRAGGLLACGVAQGA
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/protein_id="AAC31822.1"
/db_xref="GI:3342533"
                                              (bases 1 to 690)

Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.

Direct Submission
Submitted (DG-JUL-1998) Microbiology, Stockholm University,
Stockholm S-106 91, Sweden
Location/Qualifiers
            U.S.A. 95 (17), 10078-10082 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="peptidoglycan recognition protein"
a 250 c 188 g 123 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetLeupheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="bone marrow"
1. .690
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دو:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative"
                                                                                                                                                                                                                                                                                             /codon_start=1
            Proc. Natl. Acad. Sci.
98374308
to humans
                                                                                                                                                                                                                                     /gene="PGRP"
45. .635
/gene="PGRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PGRP"
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/gene="PGRP"
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   from insects
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Ratio:
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ORIGIN
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rpArgAlaLeuProSerGluCysSerSerArgLeuGlyHisProValArg
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LOCUS MMTAG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALAS
ECACHLSLPLRYVVSHTAGSSCNTPASCOQOARNVQHYHMKTLGWCDVGYNFLIGED
GLVYEGRGWNFTGAHSGHINNPMSIGISFMGNYMDRVPTPQAIRAAGGLLACGVAQGA
LRSNYVLKGHRPVQRTFLOADLYHLIQNWPHYRSP"
251 186 9 126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 724)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wan,T., Zhang,W. and Cao,X.
Direct Submission
Submitted (08-MAR-2000) Department of Immunology, Second Military
Medical University & Shanghai Brilliance Biotechnology Institute,
800 Xiangyin Rd., Shanghai 200433, P.R. China
Location/Oualifiers
1. 724
                                                                                                                                                                                                                                                                                                                                                AF242517 724 bp mRNA PRI 15-AUG-2000
Homo sapiens hypothetical protein SBBI68 mRNA, complete cds.
AF242517
142
                                                                                           509
                                                                                                                                          GGAGACAGAAGACCCGGCCTGCTGCTGCCCCATAGTGCCCCGGAACGAGT 144
                                                                                                                        143 ValSerArgGlyPheLeuArgSerAsnTyrGluValLysGlyHisArgAs 159
                                                                                                                                                                                     pValGlnSerThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
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                                                             126 alProAlaLysArgAlaLeuArgAlaAlaLeuAsnLeuLeuGluCysGly
                                                                              1 MetLeuPheAlaCysAlaLeuLeuAlaLeuLeuGlyLeuAlaThrSer..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein SBB168"
/protein_id="AAF99598.1"
/db_xref="G1:9802033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 67.196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                      erTrpGluHisTyrArg 181
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4.325
84.656
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US-09-462-625-2 x AF242517
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                                                                                                                                                                                                                                                                                                              seq_name: gb_pr:AF242517
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                                                                                                                                                                                                                                                 176
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                                                                                                                                                                                    159
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
11 (bases 1 to 4205)
Prokhortchouk, E.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-APR-1997) E.B. Prokhortchouk, Institute of Gene
Balology, Vavillova 34/5, 117334 Moscow, RUSSIA
2 (bases 1 to 4202)
Kiselev,S.L., Kustikova,O.S., Korobko,E.V., Prokhortchouk,E.B.,
Kabishev,A.A., Lukanidin,E.M. and Georgiev,G.P.
Molecular cloning and characterization of the mouse tag7 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                              TyrGluGlyArgGlyTrpAsnIleLysGlyAspHisThrGlyProIleTr 109
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J. Biol. Chem. 273 (29), 18633-18639 (1998)
98325081
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Location/Qualifiers
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WO 0129224-A 7 26-APR-2001;
                                 ZymoGenetics, Inc. (US)
Location/Qualifiers
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LOCUS AX119918 1110 bp DNA
DEFINITION Sequence 7 from Patent W00129224.
ACCESSION AX119918
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US-09-462-625-2 x MMTAG7
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TITLE
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Align seg 1/1
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JOURNAL
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231 c 300 g 252 t
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Eukamaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1128)
Conklin,D.C., Adler,D.A. and Fox,B.A.
Granulocyte peptide homolog zgpa1
Patent: WO 0129224.A. 4. 26-APR-2001;
                                                                                                    11-MAY-2001
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                                                                                                  PAT
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Location/Qualifiers
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                                       Seq_name: gb_pat:AX119915
                                                                    seq_documentation_block:
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89. .1195
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VANNSCDVAXNFLVGDDGRYYEGYOMNIQGYHTQGYNNISLGFAFFGTKKGHSPSPA
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RPLSNATLPAKYGIIITHAGRTCNISDECRLLVRDIQSFYIDRLKSCDIGYRFLVGQD
GAIYEGVGWNVQGSSTPGYDDIALGITFMGTFTGIPPNAAALEAAQDLIQCAMVKGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; I amamaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1858)
2hang, W., Wan, T. and Cao, X.
Direct Submission
Submission
Submitted (08-MAR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai Erilliance Biotechnology Institute, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 lyPheLeuArgSerAsnTyrGluValLysGlyHisArgAspValGlnSer 162
113 SerIleGlyIleThrPheMetGlyAsnPheMetAspArgValProAlaLy 129
                                                                                                                                                                                                                                                                                         163 ThrLeuSerProGlyAspGlnLeuTyrGlnValIleGlnSerTrpGluHi 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             916 GCCCTGGGCATTACCTTCATGGGCACCTTCACAGGTATACCACCAATGC
                                                                                              129 sArgAlaLeuArgAlaAlaLeuAsnLeuLeuGluCysGlyValSerArgG
                                                                                                                                                                                                                                           1016 GGTACCTGACTCCCAACTACCTGCTGGGCCACAGTGATGTGGCCCGA
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539 c 433 q 468 t
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                                                                                  Direct Submission
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Kuscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(al (bases 1 to 166867)

Koliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Conter, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Douple, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibpeyam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Murbo, T., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoc, J., Phouaneanvong, S., Pittman, G.S., Patel, S., Pfeiffer, B., Phouaneanvong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Rubin, G.M. and Venter, J.C., Sequencing of Drosophila chromosome 2R, region 44D2-44E1
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Drosophila melanogaster, chromosome 2R, region 44D2-44E1, BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 euArgAlaAlaLeuAsnLeuLeuGluCysGlyValSerArgGlyPheLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 yileThrPheMetGlyAsnPheMetAspArgValProAlaLysArgAlaL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ArgSerAsnTyrGluValLysGlyHisArgAspValGlnSerThrLeuSe 165
                                                                                                                                                                                                                                                                              893
                                                                                                                                                                                                                                                                                                                                                                                     894 ATAACTICCIGGIGGCCAGGAIGGCGCCATITAIGAAGGGGIGGGCIGG 943
                                                 744 GACCACTGTCCAGGATGACTCTCCCAGCGAAGTATGGCATCATTATCCAC 793
                                                                                                                                                                                                                                                                                                                                      86
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uCysSer.SerArgLeuGlyHisProValArgTyrValValIleSerHis
                                                                                                         49 ThralaGlySerPheCysAsnSerProAspSerCysGluGlnGlnAlaAr
                                                                                                                                                              194 ACTGCCGGGAGGACCTGCAACATTTCTGATGAGTGCCGCCTGCTGGTCCG
                                                                                                                                                                                                                                                                        344 GGACATCCAGTCTTTCTACATAGACAGGCTCAAGTCATGCGACATTGGTT
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                           Submitted (16-MAR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Mar 17, 2001 this sequence version replaced 91:5670628.
Pfeiffer, B., Poon, L., Sequeira, A., Seum, n., Serm, L.L. and Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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159571 CTTCCTGGGCAACTACCAACACCCTCACCTCTGCTCAGATCACCG 159620
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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Ferriera, S., Frise, E. Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
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Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G. M. and Venfer, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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On Apr 21, 2001 this sequence version replaced 91:6435866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC007303 169509 bp DNA INV 21-APR-2001
Drosophila melanogaster, chromosome 2R, region 44E-44F, BAC clone
BACR43104, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Berkeley, CA 94720
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CDR131676

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Description

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E16478 Bombyx mori E16479 Bombyx mori E16480 Bombyx mori AB016249 Bombyx mo AF207538 Drosophil

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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AE003526 Drosophil AE003552 Drosophil AF035445 Calpodes AC018100 Drosophil AE003558 Drosophil AC010028 Drosophil AF149838 Mus muscu AF149837 Mus muscu

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1 (bases 1 to 549) Georgiav G.P., Kiselev,S.L., Prokhorchouk,E.B. and Ostermann,E. Nucleic acid encoding tag7 polypeptide Patent: US 6172211-A 1 09-JAN-2001, 16-MAY-2001 PAT ALIGNMENTS AR124884 549 bp DNA , Sequence 1 from patent US 6172211. AR124884 AR124884.1 GI:14110245 Location/Qualifiers 1. .549 /organism="unknown" 161 c 151 g Unclassified. 117 source BASE COUNT ORIGIN FEATURES

SUMMARIES

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Matches 549; Conservative
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 669)
Slayton, W.B., Rigaa, A., Hancock, J.D., Zaugg, J.K., Le, T.V.,
Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R.
Granulocyte-colony stimulating factor up-regulates expression of
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Slayton,W.B., Rigaa,A., Hancock,J.D., Zaugg,J.K., Le,T.V.,
Trautman,W.S., Spangrude,G.J., Carroll,W.L. and Schibler,K.R.
Direct Submission
Submitted (11-007-1999) Pediatrics, University of Utah, 50 No.
                                                     atgttgtttgcctgtgctcttgcctcctgggtctggcaactcctgcagtttcatc
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Medical Drive, Room 2A126, Salt Lake City, UT 84132, USA
Location/Qualifiers
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           Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF193843 669 bp mRNA ROD
Mus musculus TAG7-like protein mRNA, complete cds.
AF193843
                                  Indels
                     1.1e-131;
           DB 6;
                               0; Mismatches
          Score 549;
Pred. No. 1
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        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 549; Conservative 0
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AUTHORS
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/translation="MLFACALLALGLATSCSFIVPRSEWRALPSECSSRLGHPVRYV
VISHTPAGSPCNSPDSCEDQARNVOHYHKNELGWCDVAXNFLLGEDGHYYEGRGWNIKG
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OSTLGSPGDLYVQUSWERVRE"
112 c 173 g 140 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 680)
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AF076482
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/db_xref="GI:6273361"
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Query Match
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     Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.
A Peptidoglycan recognition protein in innate immunity conserved
from insects to humans
                                                                                                                                                                                                                                                                                /product="peptidoglycan recognition protein precursor"
/protein_id="AAC31821.1"
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                                                            Subject 1 to 680)

Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.

Direct Submission
Submitted (08-JUL-1998) Microbiology, Stockholm University,
Stockholm S-106 91, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg
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                                      Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998) 98374308
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216 c 174 g 144 t
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Pred. No. 2.8e-131;
0; Mismatches 1;
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36. .58
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/note="PGRP"
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84. .581
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Best Local Similarity 99.8%;
Matches 548; Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: j Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3342530.
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DHTGPIWNPWSIGITFMGNFMDRVPAKRALRAÀLNLLECGVSRGFLRSNYEVKGHRDV
                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia,
                                                                                                                                                                                                                                                              12-JUL-2001
clone MGC:11430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garc:
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCL_CGAP_Mam1" /lab_host="DH10B"
  540
                                              575
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                                                                                                                                                                                                                                  BC005582 713 bp mRNA ROD Mus musculus, peptidoglycan recognition protein, IMAGE:3969014, mRNA, complete cds.
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BC005582,1 GI:13542755
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Length 713;

Score 547.4; DB 10;

99.78;

MEDLINE 98325081 COMMENT. ON JUL 6 FEATURES SOURCE Gene	CDS.	BASE COUNT ORIGIN Ouery Mat	Best Local Similaricy 99.36; Matches 546; Conservative Qy latgittiticitique content of lilililililililililililililililililili	Oy 61	Qy 241 gcctacaacttccttattggagagacggtcatt	Mus. Db 361 aacttcatggaccgggtacccgcaaagcgggccc	\$6 & \$6	ρ Λ
Dest Local Similarity 99.8%; Pred. No. 2.8e-131; Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 1 atgituate 548; Conservative 0; Mismatches 1; Indels 0; Gaps 1 atgituate 50	121 gttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcctgt 180 [241 gcctacaacttccttattggagagggcggtcatgtatgaaggccgaggctggaacatc 300 [1111111111111111111111111111111111	361 aacttcatggaccgggtaccggaaagcgggcctccgtgctgcctaaatcttctggaa 420			ORGANISM Mus muscatus Discourse Muscacos; Chordata; Craniata; Vertebrata; Euteleostomi REFERENCE L (bases 1 to 678) AUTHORS Kustikova,O.S., Kiselev,S.L., Borodulina,O.R., Senin,V.M., Afanas'eva,A.V. and Kabishev,A.A. TITLE Cloning of the tag7 gene expressed in metastatic mouse tumors JOHRNAL Genetika 32 (5), 621-628 (1996)		REFERENCE 3 (bases I to 678) AUTHORS Kiselev,S.L., Kustikova,O.S., Korobko,E.V., Prokhortchouk,E.B. Kabishev,A.A., Lukanidin,E.M. and Georgiev,G.P. TILE Molecular cloning and characterization of the mouse tag7 gene encoding a novel cytokine JOURNAL J. Biol. Chem. 273 (29), 18633-18639 (1998)

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415"
2185"
LALIGIATSCSFIVPRSEWRALPSECSSRLGHPVRYV
NVQHYKNELGWCDVAYNFLIGEDGHVYEGRGWNIKG
DRVNKAGPPCCPKSSGIWGVSGLPEIQL"
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ersion replaced g1:785010
                                                                                                                                                                                                                                  3.4; DB 10; Length 678; 1.2e-127; tches 1; Indels 2;
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15-AUG-1998

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/translation="msrrsmilawalpsilrigaaqetedpaccspivprnewkalas
scoquislikryvvshtagesscuptascoqodarnvQHYHMKTLGWCDVGYNFLIGED
GLVPGRGWHFTGAABGHLWNPMSIGISFWGNYMDRVPTPQAIRAAGGLLACGVAQGA
IRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHYRSP"
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 690)

Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.

A peptidoglycan recognition protein in innate immunity conserved from insects to humans

Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998)
98374308
                                                                                                                                                                                                                                       Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds.
AF076483 GI:3342532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="peptidoglycan recognition protein precursor"
/protein_id="AAC31822.1"
/db_xref="GI:3342533"
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Direct Submission
Submitted (08-JU1-1998) Microbiology, Stockholm University,
Stockholm 5-106 91, Sweden
                                                              440 AAAIGIGGGGTGTCTGAGGGCTTCCTGAGATCTAACTATGAGGTCAAAGGACATCGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 690;
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250 c 188 g 123 t
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Pred. No. 1.5e-71;
); Mismatches 114;
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/tissue_type="bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                 mRNA
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/gene="PGRP"
/note="putative"
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/gene="PGRP"
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77.28;
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V19HPAGSEYGSPDSCEGOARNVOLYQMKQLGWCDVAYNFLIGEDGHYYEGRGWTIK
GDHTGPIWNPMSIGITFMGDYSHRVPAKRALRAALNLLKCGVSEGFLRSNYEVRGHRD
VQSTLSPGDQLYEIIQSWDHYRE"
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                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                          I (bases 1 to 630)
Rehman,A., Teodecki,E.E. and Krueger,J.M.
Direct Submission
Submitted (25-MAY-1999) Veterinary Comparative Anatomy,
Pharmacology, and Physiology, Washington State University, P.O.
645520, Pullman, WA 99164, USA
Location/Qualifiers
Rattus norvegicus peptidoglycan recognition protein PGRP (Pgrp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ccagttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcc 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="peptidoglycan recognition protein PGRP'
/protein_id="AAF73252.1"
/db_xref="GI:8132326"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10116"
                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                     /tissue_type="spleen"
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                                           AF154114.1 GI:8132325
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20. .571
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                 mRNA, complete cds
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Best Local 3
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404 487 464

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163 231 291 283

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/product="peptidoglycan recognition protein"
/protein_id="CAC19553.1"
/db_xref="G1:11990124"
/tb_xref="G1:11990124"
/translation="MTRHCVLLVWALLALLSLGAAREDPPACGSIVPRREWRALASEC
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VYEGRGWNIKGAHAGPTWNDISIGISFMGNYWNRVPPPRALRAAQNLLACGVALGALR
SNYEVKGHRDVQPTLSPGDRLYEIIQTWSHYRA"
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Mammalia; Butheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
1 (bases 1 to 700)
Kappeler, S.R., Farah, Z. and Puhan, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kappeler, S.R.
Direct Submission
Submitted (21-DEC-1998) Kappeler S.R., Institute of Food Science,
Swiss Federal Institute of Technology, LFO F26, 8092 Zurich,
                                                                                                                                                                                                                           MAM 21-DEC-2000 peptidoglycan recognition protein.
                                                                                                                                                                 292 TGGGCTGCTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGG 351
                                                                                                                                                                                                                                                                                                  geateaectteatggggaaetteatggaeegggtaeeegeaaagegggeeeteegtgetg 403
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                 ACACCTGAGCCTGCCTTACGCTATGTGGTGGTATCGCACACGGGGGCAGCAGCAGCTGCA
                                                                                             geegeetgggggcacccagttcgctacgtggtgatctcacacacagccggcagcttctgca
                                                                       acagcccggactcctgtgaacagcaggcccgcaatgtgcagcattaccacaagaatgagc
                                                                                                                                                   tgggctggtgcgatgtagcctacaacttccttattggagaggacggtcatgtctatgaag
                                                                                                                                                                                                                                                                                                                                          412 GCATCAGCTTCATGGGCAACTACATGGATCGGGTGCCCACACCCCCAGGCCATCCGGGCAG
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25. .606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="Somali breed"
/db_xref="taxon:9838"
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Arabian camel.
Camelus dromedarius
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TITLE
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/protein_id="aAF99598.1"
/db_xxef="G1:9802033"
/tb_sxef="G1:9802033"
/tb_sxef="G1:9802033"
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ECAQHHSLALNAYVSTRAGSSCONTPASCOQOARNVOHYHMKTLGWCDVGYRFLIGED
GLYYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGA
LRSNYLKGHRDVQRTLSPGNOLYHLIQNWPHYRSP"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Man, T., Zhang, W. and Cao, X.

Direct Submission
Submitted (08-MAR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 xiangyin Rd., Shanghai Brilliance Biotechnology Institute, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cctcctgcagtttcatcgtgcccgcagtgagtggagggccctgccatccgagtgctcta 103
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                                                                                                                                                                                                                                                                    gcatcaccttcatggggaacttcatggaccgggtacccgcaaagcgggccctccgtgctg 403
                                                                                                                                                                                                                                                                                                                                                                                                                          aaggacaccgggatgtgcaaagcactctctccaggtgaccaactctatcaggtcatcc 523
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGGGGGGCAGCAGCTGCA 246
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                                     tgggctggtgcgatgtagcctacaacttccttattggaggaggacggtcatgtctatgaag
                                                                                                                                                                                             gccgaggctggaacatcaagggtgaccacacagggcccatctggaatcccatgtctattg
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Pred. No. 1.5e-71;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
30. .620
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Local Similarity 77.2%;
les 385; Conservative
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Best Local S
Matches 385
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DEFINITION

AF242517

RESULT

ACCESSION KEYWORDS SOURCE

VERSION

524

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

source

FEATURES

CDS

BASE COUNT

44

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523

591

471 463

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae, Drosophila.

E (Dases 1 to 166867)
E (Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Roders,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Ferifera,S., Frise,E., Galle,R.F., Gargi,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACUU7085 166867 bp DNA INV 17-MAR-2001
Drosophila melanogaster, chromosome 2R, region 44D2-44E1, BAC clone
BACKISHIO, complete sequence.
                                                                                                                                                                                                                                                                                                                                                      /translation="MLFACALLALGLATSCSFIVPRSEWRALPSECSSRLGHPVRYV
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Pred. No. 2.9e-54;
0; Mismatches 6; Indels
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1157 c 1020 g 1003 t 12 othe
                                            /db_xref="taxon:10090"
/map="A3 cytogenetic band"
3507. .3818
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/db_xref="SPTREMBL:Q62185"
                                                                                                                                                                                                                                                                                                      /protein_id="CAA72803.1"
                                                                                                                                                                                                                                                                                        protein"
                                 strain="B6/CBAFIJ"
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/product="TAG7
                                                                                                         /gene="tag7"
/533. .>3818
/gene="tag7"
/gene="tag7"
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AC007085.7 GI:13374639
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/gene="tag7"
3507. .3513
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/gene="tag7"
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Best Local Similarity 97.7%;
Matches 253; Conservative
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Sciurognathi; Muridae; Murinae; Mus.
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J. Biol. Chem. 273 (29), 18633-18639 (1998)
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Submitted (01-APR-1997) B.B. Prokhortchouk, Institute of Gene
Bloidogy, Vavilova 34/5, 117334 Moscow, RUSSIA
2 (bases 1 to 4205)
                                                                                                                                                    Gaps
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                                                                                                                Length 700;
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                                                                                                                                                  0; Mismatches 122;
                                                                                                                  DB 4;
                                                                                                               Score 307.8; DB Pred. No. 2.9e-69
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1. 4205
/organism="Mus musculus"
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Mammalia, Eutheria, Rodentia,
1 (bases 1 to 4205)
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                                                                                                                56.1%;
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tag7 gene.
house mouse.
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247 c
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                                                                                                                               Best Local Similarity 75.7
Matches 381; Conservative
                               678.
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BASE COUNT
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Best Local 3
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COMMENT
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417 ggaatgtggggtgtctcgggggcttcctgagatccaactatgaagtcaaaggacaccggga 476
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-MAR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Mar 17, 2001 this sequence version replaced gi:5670628. Sequence submitted by:
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/clone_lib-"RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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               Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
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Lawrence Berkeley National Laboratory, MS 64-121
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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Pred. No. 5e-24;
0; Mismatches 209;
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Best Local Similarity 56.0%;
Matches 270; Conservative
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                                                                                                                                     Unpublished
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Pureryota, Neoptera, Endopteryota; Diptera; Brachycera; Petrygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

E. (bases 1 to 169509)
E. (celliker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Rolars, C.S., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Roles, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farise, E., Galle, R.F., Garg, N.S., George, R.A., Ferrieras, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Ibeyam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Pacleb, J., Paragas, V., Park, S., Patland, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Savoet, J.S., Smith, H.O., Rubin, G.M. and Venter, J.G. Sequencing of Drosophila chromosome 2R, region, 44E-44F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley
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Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Clavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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DD 159637 CTCCGATGCGGTCAGTCGCGGCCAGATCGTTTCCGGATACATCCTGTACGGACATCGGCA 159696
                                                                                                                       DD 159697 GGTCGCTCCACCGAGTGCCCCGGCACCAACATCTGGAACGAGATCCGCACTGGTCCAA 159756
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                                                                                  477 tgtgcaaagcactctctccaggtgaccaactctatcaggtcatccaaagctgggaaca
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Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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/db_xref="taxon:7227"
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BACR43104, complete sequence.
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IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                       Db 105623 GGGCAACTACAATACCAACACCCTCACCTCTGCTCAGATCACCGCTGCCAAGGGTCTGCT 105564
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                                                                                                                                                                                                                                                                                                                                    177 ctgtgaacagcaggcccgcaatgtgcagcattaccacaagaatgagctgggctggtgcga 236
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                                                                                                                                                                     Gaps
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* This sequence will be replaced
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/clone="BACR43104 (D581)"
Cclone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophia melanogaster BAC library, partial EcoRI
pBACe3.6)"
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Pred. No. 5e-24;
0; Mismatches 209;
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                                                                BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 cccagttcgctacgtggtgatctcacacacagcggcagcttctgcaacagcccggactc 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 catcgtgccccgcagtgagtggagggccctgccatccgagtgctctagccgcctggggca 116
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 ctgtgaacagcaggcccgcaatgtgcagcattaccacaagaatgagctgggctggtgcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150371 CTGCATCACACAGCTGCAGAACATCCAGGCCTACCACATGGACTCCCTGGGCTGGGCTGGGCCGA
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                                                                                                                                                                                                                                                                                                                                                                                       Length 172838;
1. .172838
/organism-brosophila melanogaster"
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| 38482 c 38368 g 47957 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                       Score 131.6; DB Pred. No. 5e-24;
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56.0%;
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KLTYDSVQEMPYLDQVVAETLRKYPILPHLLRRSTKEYQIPNSNLILEPGSKIIIPVH
                                                                                                                                                                                                                                                                              LECNSLODPSAEFROKGREIFTRRRHSTLVOSFIFTNARLARKLRIKVLPDDLTOFFM
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FFVAGFETSSSTMSLCLYELALQPDIQQRLREEIESVLANVDGGELNYDVLAOMTYLD
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DPHLYPHPKLFDSSRLKAYKSNSRHPFAYLPFGTFGPRSCIGLRFGKWQAKIGIVSAL
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complement(join(<30499. 30823,30901. 31084,31413. 316
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/db_xref-"FLYBASE:FBan0033305"
/db_xref-"FLYBASE:FBan0033305"
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complement(join(30499. .30823,30901. .31084,31413. .31618,
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Pred. No. 4.7e-24;
0; Mismatches 209; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="CG14748 gene product"
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Best Local Similarity 56.0%;
Matches 270; Conservative
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n /rpt_family="(TGAA)n"

complement(177. .453)

/rpt_family="Aluab"

complement(472. .712)

/rpt_family="Aluab"

n complement(472. .712)

/rpt_family="MIR"

/46. .904

/note="DDS similarity to overlapping ESTS:

N39722 yx92e04.rl Homo sapiens CDNA clone 269214 5';

(12. .170); 994 identity.-AA283147 ztl4007.rl NCI_CGAP_GCBI Homo sapiens CDNA clone IMAGE:713101 5'; (6. .163); 994 identity.-AA143160 z149407.rl Soares pregnant uterus NDHPU Homo sapiens CDNA clone 184625; (1. .43); 100% identity.-AA142881 z149407.rl Soares pregnant uterus NDHPU Homo sapiens CDNA clone 505261 5'; (1. .43); 100% identity.-AA142881 z149407.sl Soares pregnant uterus NDHPU Homo sapiens CDNA clone 505261 3'; (570. .527); 64% identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4.419 of this accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from bases 146,203 to 166,500. Additional chromosome 19 map and sequence information may be obtained at:
http://www.bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                Butaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 166500)
Lamerdin,J.E., McCready,P.M., Richardson,P., Sakaldasis,G.,
Burkhart-Schultz,K., Gordon,L., Scott,D., Johnson,G., Stilwagen,S.,
Burkhart-Schultz,K., Gordon,L., Regala,W., Terry,A., Danganan,L.,
Erler,A., Christensen,M., Georgescu,A., Avila,J., Attix,C.,
Andreise,T., Amico-Keller,G., Coeffield,J., Duarte,S., Lucas,S.,
Bruce,R., Thomas,P., Quan,G., Krommiller,B., Arellano,A.,
Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and
Carrano,A.V.
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Hypothetical CDS constructed from overlapping ESTs and
Xgrail predictions. EST coverage is lacking for some
portions of the CDS. Gene may be alternatively spliced, as
multiple transcripts map into this region; alternatively,
these individual clones may represent artifactual events
during RT and cDNA creation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence analysis of a 2.5 Mb region in 19q13.2-13.3 between APOE
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12784. .12994,13080. .13162,13903. .13958,14053. .14128,
14429. .14568,14726. .14804,14982. .15039,15813. .15885,
AC007785 166500 bp DNA PRI 11-JUN-1999
Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19), complete
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70. 145
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                                                                                                                                              ELGRLQGLDGQNTRDTRENEIWHLREQVSRLASEKRELEAĞLGRSREEALAGRAARQE
BABLRGLVRGLELELRQERGGLGHRYWAGRRGQDCRRLAKRLESAKASERSLRARKIYLIT
SELALY KRGGRGSRGRRGRPARPSPSTGGRALRFDFTAFVKAKERKQREI JOMKOQORN
RLGSGGGGGGSGDGPSVSWSRQTQPPAALTGRGDAPNRSRNRSSSVDSFRSRCSSASSCSDL
                                                                                                                                                                                                                                   EDFSESLSRGGHRRRGKPPSPTPWSGSNMKSPPVERSHHQKSLANSGGWVPIKEYSSE
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5875. .5898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 100.000" complement(6148. .6443) /rpt_family="AluSx"
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complement(200. 2185)
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complement(2747. 3044)
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20674 CCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCC 20615
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12847, 12908
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Pred. No. 7.8e-23;
0; Mismatches 50; Indels
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complement(10753. .11057)

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complement(11065. .11191)

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9909. .9944
/rpt_family="MER5B"
/rpt_family="MER5B"
/rpt_family="MER5B"
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complement(12186. .12327)
/rpt_family="LiM1"
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Best Local Similarity 75.8%;
Matches 157; Conservative (
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Search completed: December 17, 2001, 09:36:51 Job time: 6531 sec

AF242517 AC007785 AC091505 RNCAST5 AF346597 RNCAST3

RSCALPST AF346598 RNCAST2 AL392105

RNCAST1

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AF193843 Mus muscu AF076482 Mus muscu BC005582 Mus muscu

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AR124884

DB

Length

Query Match 1

2

AF154114 CDR131676

AF076483

AR124884 Sequence

Description

X86374 M.musculus

7.13588 Rattus norv AL392105 Human DNA AL390251 Homo sapi AC016474 Homo sapi AC021399 Homo sapi AC023169 Homo sapi AC023169 Homo sapi AC031479 Homo sapi AC033048 Mus muscu AC033048 Mus muscu AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi AC033048 Homo sapi

AB002323 Human mRN L08505 Rattus norv AY004877 Mus muscu D13896 Rat mRNA fo

ABO02323 RATDYNEINC AYO04877

14351 15500 31934

AB007974

3.6 184452 3.6 187174 3.6 193889 3.6 202655 3.6 222016 3.5 1159 3.5 3580

Homo sapi Homo sapi

U64859 Cae AC005075 H AC068791 H AC073866 H AP000909 H

AL596265

ALIGNMENTS

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Result
                                                                                                    Search time 1569.57 Seconds
(without alignments)
5770.339 Million cell updates/sec
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                       December 17, 2001, 08:42:11
                                                                        nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_htg_rod:*
em_htg_other:*
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em_htgo_inv: *
em_htgo_rod: *
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Maximum DB seq length: 200000000
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1 (bases 1 to 549)
Georgiev.G.P., Kiselev,S.L., Prokhorchouk,E.B. and Ostermann,E. Nucleic acid encoding tag7 polypeptide Nucleic acid encoding tag7 polypeptide Patent: US 6172211-A 1 09-JAN-2001; 16-MAY-2001 PAT 4 120 AK124884 549 bp DNA Seguence 1 from patent US 6172211. AR124884 Location/Qualifiers
1. .549
/organism="unknown"
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SUMMARIES

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Query Match

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Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 680)
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100.0%; Pred. No. 0;
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Best Local $
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 669)
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Mus musculus TAG7-like protein mRNA, complete cds.
AF193843
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                       DB
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                    100.0%; Score 549; 100.0%; Pred. No. 0;
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Matches 549; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

PEATURES

JOURNAL REFERENCE AUTHORS

TITLE

DEFINITION

AF193843 LOCUS

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Query Match
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GSTLSPGDQLYQVIOSWEHYRE"
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Kang, D., Liu,G., Lundstrom,A., Gelius,E. and Steiner,H.
A peptidoglycan recognition protein in innate immunity conserved
from insects to humans
Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998)
98374308
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                                                                 2 (bases 1 to 680)
Mang, D. Liu, G., Liundstrom, A., Gelius, E. and Steiner, H.
Direct Submission
Submitted (08-JUL-1998) Microbiology, Stockholm University,
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1. .680
                                                                                                                                     Location/Qualifiers
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/translation="MLFACALLALIGIATSCSFIVPRSEWRALPSECSSRLGHPVRYV
VISHTAGSFCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKG
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 3342530.
Location/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 713)
Strausberg,R.
                                                                                                                                                                                                                                                                                         713 bp mRNA ROD 12-JUL-2001 MAG mus musculus, peptidoglycan recognition protein, clone MGC:11430 BC005582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing center
Conter code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contert villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garc.
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
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576 CGAGAGTGA 584
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Length 713;

DB 10;

Score 498;

90.78;

MEDLINE 98325081 COMMENT On Jul 6, 1995 this sequence ERATURES 1. GOR SOURCE / Organism="Mus mus / Strain="A,Sn" / Ab_xref="taxon:10" /	CDS / Gene="tagy" / Gene="tagy" / Gene="tagy" / Codon_start=1 / Protein_id="CAA66 / Ab_xref="AG1.88755 / Ab_xref=	ORIGIN Query Match Best Local Similarity 100.0%; Score Bact Local Similarity 100.0%; Prec Matches 379; Conservative 0; M QY 1 atgrtgtttgcctgtgctctccttgcccf	Oy 61 gtgcccgcagtgagtgagggcctgcc	156 181 216 241 276	Oy 301 aagggtgaccacacacatctggar 	RESULT 6 MWTAG7 4205 bp DNI LOCUS DEFINITION Mus musculus tag7 gene, ex ACCESSION Y12088 VERSION Y12088.1 GI:2765147 KEYWORDS tag7 gene. SOURCE house mouse. ORGANISM Mus musculus ENKATYOLS Mus musculus BOKATYOLS Mus musculus BOKATYOLS Mus musculus BOKATYOLS Musmalia; Eutheria; Rodent. 1 (bases 1 to 4205) AUTHORS Prokhortchouk, E.B. TITLE Direct Submission JOURNAL SUbmitted (01-APR-1997) E.1
Best Local Similarity 99.8%; Pred. No. 2.7e-279; Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 addtgtttgcctgtgctcccttgccccctgggtctggcaacctcctgcagttcatc 60	Oy 121 gttcgctacgtggtgatctcacacacagcggcagcttctgcaacagcccctgt 180	Oy 301 aagggtgaccacacagggcccatctggaatcccatgtctattggcatcaccttcatgggg 360	467 481 527 541	ύ-Ü ν z	X86374.1 GI: tms1 gene. house mouse. Mus musculus Eukaryota; Me Mammalia; Eut I (bases 1 I Kustikova,O.S	TITLE Actioning of the tag7 gene seed in metastatic mouse tumors JOURNAL MEDLINE 9532104 ACTIONING Of the tag7 gene seed in metastatic mouse tumors JOURNAL Senetika 32 (5), 621-628 (1996) ACTHORS RUSTIAN Academy, 0.S. TITLE JULE OLIVER (18-APR-1995) 0.S. Kustikova, Inst of Gene Biology RUSSIA RUSSIA AUTHORS AUTHORS RISSIA AUTHORS ALSENEV.A.A., Lukanidin.E.M. and Georgiev.G.P. KADIShev.A.A., Lukanidin.E.M. and Georgiev.G.P. TITLE MOlecular cloning and characterization of the mouse tag7 gene encoding a novel cytckine JOURNAL J. Biol. Chem. 273 (29), 18633-18639 (1998)

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11:107415"

4BL:Q62185"

ABL:Q62185"

APRICALIALIGIATSCSFIVPRSEWRALPSECSSRLGHPVRYV

SEQARNVQHYKNELGWCDVAXNFLIGEDGHVYEGRGWNIKG

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nce version replaced gi:785010.
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peptidoglycan recognition protein.
Arabian camel.
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//db_xref="SPTERBEL:062185"
/translation="MLFACALLALLGLATSCSFIVPRSEWRALPSECSSRLGHPVRYV
VISHTAGSFCNSPDSCEQQARNVQHYHKNELGWCDVAY"
a 1157 c 1020 g 1003 t 12 others
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus norvegicus peptidoglycan recognition protein PGRP (Pgrp)
Biology, Vavilova 34/5, 117334 Moscow, RUSSIA.
2 (bases 1 to 4205)
Kiselev,S.L., Kustikova,O.S., Korobko,E.V., Prokhortchouk,E.B.
Kabishev,A.A., Lukanidin,E.M. and Georgiev,G.P.
Molecular cloning and characterization of the mouse tag7 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                       encoding a novel cytokine
J. Biol. Chem. 273 (29), 18633-18639 (1998)
98325081
                                                                                                                                                                                                        /map="A3 cytogenetic band"
3507. .3818
                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA72803.1"
/db_xref="G1:2765148"
                                                                                                                                                            /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                      protein"
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                                                                                                                Related entry: X86374.
Location/Qualifiers
1. .4205
                                                                                                                                                                            /strain="B6/CBAFIJ
                                                                                                                                                                                                                                                                                                                                                                                                      /product-"TAG7
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                                                                                                                                                                                                                                            /gene="tag7"
3533. .>^^
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3507. .3513
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/gene="tag7"
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3533. .3
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Rehman, A., Teodecki, E.E. and Krueger, J.M.
Direct Submission
Submitted (25-MAY-1999) Veterinary Comparative Anatomy,
Pharmacology, and Physiology, Washington State University, P.O. Box 646520, Pullman, WA 99164, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to Homo sapiens and Mus musculus
peptidoglycan recognition protein; similar to Trichoplusia
ni and Mus musculus TAG7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"peptidoglycan recognition protein PGRP"

/protein_id="AAR73251."

/db_xref="GI:8132326"

/translation="MLPAWAPFPALLGLADSCCFVVPRSEWKALPSECSKGLKKPVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVISHTAGSFCSSPDSCEQQARNVQLYQMKQLGWCDVAYNFLIGEDGHVYEGRGWTIK
GDHTGPIWNPWSIGITFWGDYSHRVPAKRALRAALNLLKCGVSEGFLRSNYEVKGHRD
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Kappeler,S.R., Farah,Z. and Puhan,Z.
Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan Recognition Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDR131676 700 bp mRNA MAM 21-DEC-2000
Camelus dromedarius mRNA for peptidoglycan recognition protein
AJ131676
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/product="peptidoglycan recognition protein"
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Pred. No. 9.4e-12;
0; Mismatches 0; Indels
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25. .606

    .700
    /organism="Camelus dromedarius"

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Query Match
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Matches 22; Conservative
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Scoghisliptryvyshtagesscniptascogodarnvohymmylgwcdygyrbliged
Glyyegrgnnfleghlwnpmstgispmonymdryptpgairaagellacgvagga
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VYEGRGWNIKGAHAGFTWNPISIGISFWGNYNNRVPPPRALRAAQNLLACGVALGALR
SNYEVKGHRDVQPTLSPGDRLYEIIOTWSHYRA"
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A peptidoglycan recognition protein in innate immunity conserved
from insects to humans
Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998)
98374308
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/protein_id="AAC31822.1"
/db_xref="GI:3342533"
                                                                                                                                                                                                                                                                                                                                                                       AF076483 690 bp mRNA PRI 15-AUG-1998
Homo sapiens peptidoglycan recognition protein precursor (PGRP)
mRNA, complete cds.
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Direct Submission
Submitted (08-JUL-1998) Microbiology, Stockholm University,
Stockholm S-106 91, Sweden
Location/Qualifiers
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a 250 c
                                                                                            25. .87
88. .603
/product-"peptidoglycan recognition protein"
678. .683
                                                                                                                                                                                                                      Query Match
4.7%; Score 26; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 26; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 690)
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/note="putative"
105. .632
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/codon_start=1
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/gene="PGRP"
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45. .635
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 166500)
1 (bases 1 to 166500)
1 Lamerdin, J. E., McCready, P.M., Richardson, P., Sakaldasis, G., Burkhart-Schultz, K., Gordon, L., Scott, D., Johnson, G., Stilwagen, S., Phan, H., Velasco, N., Dol., Regala, W., Terry, A., Danganan, E., Andreise, T., Amico-Keller, G., Coefield, J., Avila, J., Attix, C., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A. S. and Carrano, A.V.
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ECAQHISLPIRYVVSHTAGSSCNPASCOQOARNVQHYHKKTLGWCDVGYRFLIGED
GLYEGRGWNFTGAHSGHLWNPMSIGISFMGNWDRVPTPQAIRAAGGLLACGVAQGA
GLRSNYVLKGHRDVGTESPGROLYHLIGNWPHYRSP"
251 c 186 g 126 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
Wan, T., Zhang, W. and Cao, X.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-MXR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC007785 166500 bp DNA PRI 11-JUN-1999
Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19), complete
                                                                                                                                                                                                                                         Homo sapiens hypothetical protein SBBI68 mRNA, complete cds. AF242517.1 GI:9802032
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Score 22; DB 9; Length 690;
Pred: No. 0.31;
0; Mismatches 0; Indels
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/db_xref="taxon:9606"
30. .620
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100.08;
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                                                                                                    GI:5042403
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Best Local Similarity 100.
Matches 22; Conservative
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complement (4789. 5083)

/rpt_family="Alusx"

re 5875. 5898

/note="DDS similarity to N28707 yx66dll.rl Homo sapiens cDNA clone 266709 5'; (223. .246); 100% identity."

6875. 5972

/note="DDS similarity to overlapping ESTS:
N39722 yx32e04.rl Homo sapiens cDNA clone 269214 5'; (439. .506); 71% identity.-AA143160 z149407.rl Soares prequant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (282. .379); 100% identity.-AA142881 z149407.sl Soares prequant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (274. .175); 95% identity."

5906. .6036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N39722 yx92e04.11 Homo sapiens cDNA clone 269214 5';
C356. 438); B18 identity.-AA283147 z114d07.r1
NCL_CGAP_CGB1 Homo sapiens cDNA
Clone IMAGE.713101 5'; (248. 400); 99% identity.-AA143160
z149d07.r1 Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 505261 5'; (127. 281); 97% identity.-N28707
yx66d11.r1 Homo sapiens cDNA clone 266709 5'; (67. 222);
98% identity.-AA142881 z149d07.s1 Soares pregnant uterus
hibppu Homo sapiens cDNA clone 505261 3'; (437. 275); 97%
identity."
     clone 505261 5'; (44. .126); 100% identity.-N28707 ys. ys. dill.1 Homo sapiens cDNA clone 266709 5'; (1. .66); 98' identity.-AA142881 zl49607.sl Soares pregnant uterus NDHPU Homo sapiens CDNA clone 505261 3'; (526. 438); 82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family-"MER64"
3841. 4060
/rpt_family-"MER64"
4294. 4451
/note-"DDS similarity to overlapping ESTS:
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complement'inf
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                                                                                                                                                                                                                                                        complement(2040. 2185)
/rpt_family="LINE2"
complement(2200. 2498)
/rpt_family="Alues"
complement(2576. 2746)
/rpt_family="Aluesgyx"
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/rpt_family="(CA)n"
complement(1673. .1973)
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2747..3044)
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/rpt_family="MIR"
complement (7538. .7639)
/rpt_family="(CA)n"
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complement(6608. 6
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complement(9539. .90
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9456. .9520
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/rpt_family="MER5B"
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N39722 yx92e04.rl Homo sapiens CDNA clone 269214 5';
(12. 170); 99% identity.-AAA83147 zti4d07.rl NCI_CGAP_GCB1
Homo sapiens CDNA clone IMAGE:713101 5'; (6. 163); 99%
identity.-AA143160 z149607.rl Scares pregnant uterus NbHPU
Homo sapiens CDNA clone 505261 5'; (1. 43); 100%
identity.-AA142881 z149607.sl Scares pregnant uterus NbHPU
Homo sapiens CDNA clone 505261 3'; (570. 527); 64%
                                                                                                      Lamerdin,J.E.
Direct Submission
Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4,419 of this accession, and overlaps BAC 264576 (CIT-B-297NI4; AC006262) from bases 146,203 to 166,500. Additional chromosome 19 map and sequence information may be obtained at:
http://www-bio.lhi.gov/bbr/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16025. .16122)
Actoe="Hypothetical arginine-rich gene product;" Hypothetical CDS constructed from overlapping ESTs and Xgrall predictions. EST coverage is lacking for some portions of the CDS. Gene may be alternatively spliced, as multiple transcripts map into this region; alternatively these individual clones may represent artifactual events during RT and CDNA creation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 62.000-DDS similarity to
overlapping ESTs:
N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
(171. .255): 95% identity.-AA283147 zt14007.rl
NCI_CGAP_CED1 Homo sapiens cDNA
clone IMAGE:713101 5'; (164. .247): 92% identity.-AA143160
z149407.rl Soares pregnant uterus NDHPU Homo sapiens cDNA
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/product-"BC282485_1"
/protein_id="AAD38244_1"
/db_xref="G1:5042405"
/translation="HLAMDOPAGLOVDYVFRGVEHAVRVMVSGQVLELEVEDRMTADQ
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MGGRPGSLAPRSAQLNSKRYLILIXSVEFDRIHYPLPLPYQGKPDPVVLQGIIRSLKE
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SELALYKRGGRGSRGRRPARPSPSPTGGRALRFDPTAFYKAKERKQRETQMKQQQRN
RLGSGGSGDGPSYSWSRQTQPPAALTGRGDAPNRSRNRSSSYDSFRSRCSSASSCSDL
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  Sequence analysis of a 2.5 Mb region in 19q13.2-13.3 between APOE and C5R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(<746. .904,1157. .1239,4294. .4451,5875. .6036,
12784. .12994,13080. .13162,13903. .13958,14053. .14128,
14429. .14568,14726. .14804,14982. .15039,15813. .15885,
16025. .16122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="19q13.3 between DM and c5R1"
//clone_lib="Cal Tech CIT-B BAC library"
//note="LLNL clone name: BC282485"
70. 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(177. .453)
/rpt_family="AluJb"
complement(472. .712)
/rpt_family="MIR"
746. .904
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/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TGAA)n"
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                                                       Unpublished
2 (bases 1 to 166500)
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TITLE
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Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (19-MAY-1997) R. De Tullio, University of Genova,
Institute of Biochemistry, Viale Benedetto XV, 1, Genova, 16132,
                  Green, E.D.

Direct Submission

Direct Submission

Submitted (18-AUG-2001) NIH Intramural Sequencing Center, 8717

Grovemont Circle, Gaithersburg, MD 20877, USA

On Aug 18, 2001 this sequence version replaced g1:13811903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNCASTS 606 bp mRNA ROD 24-FEB-1998
Rattus norvegicus mRNA for calpastatin, clone RNCAST23.
Y13591
                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features section.
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                                                                                                                    Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP44"31621"
/clone=lib="RP44"
26986. 27081
/note="single clone coverage"
48857. 48891
/note="single clone coverage"
58401. 58456
/note="single clone coverage"
65003. 65435
/note="single clone coverage"
54602 c 51545 g 38766 t
                                                                                                                                                                         Pred. No. 1.2;
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/organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                        Center clone name: 331G21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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(bases 1 to 188095)
                                                                                                                                                           Center code: NISC
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De Tullio, R.
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                      12895. ...12994
/note="DDS similarity to AA765166 nz79c05.s1 NCL_CGAP_GCB1
Homo sapiens cDNA clone IMAGE:1301672; (222. .123); 97%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 188095)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Legaspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Masirian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Zhang, L. - and Green, E. D.
                                                                                                                                                                                                                                                                                                                        r.curcted exon, program: grail2exons_human_1.3,
1, quality: excellent, score: 92.000"
12908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="GC_rich"
13080. .13162
/note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 100 000-DDS similarity to AA765166 nz/9c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301672; (122. .48); 100%
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Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Sus scrofa clone RP44-331G21, complete sequence.
AC091505
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0.32;
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                                                                                                                                                                                        /rpt_family"AT_rich"
/rpt_family"AT_rich"
complement(12186, .12327)
/rpt_family"LiM1"
complement(12334, .12384)
/rpt_family"LINE2"
                                                                                                             /rpt_family="Ar_rich"

complement(11914. .11976)

/rpt_family="Alus"

complement(12055. .12088)

/rpt_family="Alus"
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  complement(11065, .11191)
/rpt_family="AluJ"
11322, .11619
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                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="GC_rich"
12895. .12994
                                                                                                 /rpt_family="AT_rich" complement(11864. .11:
                                                              'rpt_family="AluSg'
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Best Local Similarity
Matches 22; Conserv
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/db_xref="GI:13540320"
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/gene="CAST"
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Best Local Similarity 100.
Matches 20; Conservative
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Rattus norvegicus
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PSADGESVAGGVTVATASDKVVVKKKEKKSLTPTLPMESTLNKLSDKSGVNAALDDLI
DTLGECEDTNKDDPPYTGPVVLDPMDSTYLEALGIKEETIPPEYRKLLEKNEAITGPL
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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2 (bases I to 1789)
Risbood, M.P., Lin, H. and Lee, T.
Direct Submission
Submitted (06-FEB-2001) Blochemistry, SUNY at Buffalo, 3435 Main
Street, Buffalo, NY 14214-3000, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Rattus norvegicus clone 1 calpastatin mRNA, complete cds.
AF346597
              De Tullio, R., Sparatore, B., Salamino, F., Melloni, E. and
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Risbood,M.P., Lin,H. and Lee,T.
Hypoxic induction of two rat cardiac calpastatin cDNAs
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                                          Rat brain contains multiple mRNAs for calpastatin
FEBS Lett. 422 (1), 113-117 (1998)
98133328
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                                                                                                                                                                                                                                                                                             /product="calpastatin"
/protein_id="CAA73919.1"
/db_xref="G1:2765346"
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                                                                                                                                     /strain="Sprague Dawley"
/db_xref="taxon:10116"
/dev_stage="adult"
/tissue_type="brain"
/clone="RNCAST23"
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/proteln_id="AAK29411.1"
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/db_xref="taxon:10116"
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6. .1787
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18. .548
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 (bases 1 to 606)
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Best Local Similarity 100.1
Matches 20; Conservative
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                                Pontremoli,S.
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PWDSTYLEALGIKEGTIPPEYRKLLEKNEAITGPLPDSPKPMGIDHAIDALSSDFTCS
SPTGKQTBKEKSKSTGESSKAGAGAGVTRASAVPPOPERRKVEEEVMOQALGALGDSLGTR
OPDPQSHLHAQAKOVREARAREEROEKGEBDDTVPAARTKVEDKPWOQALGALGDSLGTR
OPDPQSHLHAQAKOVREARAREEROEKGEBDDTVPAARTKVEDDAVETLARSLGTRKEDPE
DKSLUDKVRYREARREDHEKAGEREETI PPDYRLLEIVKDKORDPLLDARSLGTRKEDPE
DDFLLLDALGODFSSPANILISJGFEDAKLSAAVSETVSOVPAPSNHTAAPPPGTERROR
ELDDALDELSDSLGQRQPDPDENKPLDDKVKEKIKAEHSEKLGERDDTIPPEYRHLLD
NGGKNPERKFTAKTREKFGODPIDALSEDLDSCPPTTETSONTTKEKGKKTSSKA
SKNEEKTROSSKKTESVPKRYVDEDAT"

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QPDPQSHLRQAKQVREAKAKEERQEKCGEDEDTVPARYRLKPAKDKOGKPLLPEPEET
SKCLSESELIGELSADFVQPTYQEKPSMPAAKIKKGVVPDDAVETLARSLGTRKEDPE
DEKSLVDKVKEKAKEEDHEKLGEKEEAIPPDYRLEIVKDKDGKPLLPKEAEEQLPPLS
/translation="MSTTGAKAVKIESEKSQSSEPPVIHEKKPKGKPKEGSETKFQDA
PSADGESVAGGVTVATASDKVVVKSGVNAALDDLIDTLGECEDTNKDDPPYTGPVVLD
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PMDSTYLEALGIKEGTIPPEYRKLLEKNEAITGPLPDSPKPWGIDHAIDALSSDFTCS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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De Tullio, R.
Derect Submission
Submitted (19-MAY-1997) R. De Tullio, University of Genova,
Institute of Biochemistry, Viale Benedetto XV, 1, Genova, 16132,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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De Tullio,R., Sparatore,B., Salamino,F., Melloni,E. and
Pontremoli,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%; Score 20; DB 10; Length 1789; 100.0%; Pred. No. 4.6; ive 0; Mismatches 0; Indels
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FEBS Lett. 422 (1), 113-117 (1998)
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/organism="Rattus norvegicus"
/Astrain="Sprague Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="calpastatin"
/protein_id="CAA73917.1"
/db_xref="GI:2765342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/clone="RNCAST107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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DDFLLGALSQDFSSPANILSLGFEDAKLSAAVSETVSQVPAPSNHTAAPPPGTERRDK
ELDDALDELSDSLGGRQPDPDENKPLDDKVKEKIKAAHSEKLGERDDTIPPEYRHLLD
NDGKDVPPERPLTKNTEKPGQDQDPIDALSEDLDSCPPTTETSONTTKEKGKKTSSSKA
SKNEEKTKDSSKTEEPVPKPVDDDAT"
391 c 457 g 369 t
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641 BASE COUNT ORIGIN

Query Match 3.6%; Score 20; DB 10; Length 1858; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 20; Conservative 0; Mismatches 0; Indels 0

0;

Gaps

; 0

ò QQ

Search completed: December 17, 2001, 10:29:17 Job time: 6426 sec

Antimicrobial peptide; antibiotic; antibacterial; antifung fungicide; antiprotozoa; protozoacide; antiviral; virucide murine granulocyte peptide A; MGP-A; preservative; sepsis; endotoxaemia; mouse; 8s.

/transl_except= (pos:561..563, aa:Trp) 543..578 /*tag= b

mat_peptide

/product- MGP-A

W09729765-A1

21-AUG-1997

97WO-US02218

13-FEB-1997;

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CALIFORNIA

(REGC) UNIV 16-FEB-1996;

Selsted ME;

WPI; 1997-424753/39. P-PSDB; AAW23723

Location/Qualifiers 36..581 /*tag= a

Mus musculus

Key

2

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the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head overce or fibro-sarcomas), melanoma or leukaemia; and as a molecular apoptosis. The tag7 Dolypeptide inhibits tumour growth and induces mapping and detection of tag7 gene expression, and as probes for gene against tag7 are used as reagents for detecting tag7; as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour from the tag7 coding sequences are also useful as probes for gene against tag7; for isolating tag7 and therapeutically to inhibit or delay tumour from the tag7 coding sequences.
                                                         This sequence encodes the murine tag? of the invention.
the tag? DNA sequence are used to express recombinant ta
Claim 3; Fig 1; 138pp; English.
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Sequence 549 BP; 117 A; 161 C; 151 G; 120 T; 0 other;

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Gaps
                                                               gigececgcagigagigagggeetigecatecgagigetetageegeetiggggeacea 120
                                                                              gtgccccgcagtgagtggaggccctgccatccgagtgctctagccgcctggggcaccca 120
                                                                                             gttcgctacgtggtgatctcacacacagccggcagcttctgcaacagcccggactcctgt 180
                                                                                                     240
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                                                                                                                                                                                                                                                      tgtggggtgtctcggggcttcctgagatccaactatgaagtcaaaggacaccgggatgtg
                     ;
0
     Length 549;
                    0; Indels
100.0%; Score 549; DB 20;
100.0%; Pred. No. 8.7e-156;
Live 0; Mismatches 0;
                Conservative
       Best Local Similarity
Matches 549; Conserv
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This cDNA sequence encodes the precursor (see AAW23723) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAW3725). It was solvine BGP-A cDNA (see AAW3725). It was solvine BGP-A cDNA (see AAW3725). It was comprises signal peptide A or MGP-A (see AAW3725). It was comprises signal peptide and propeptide sequences followed by 12 C-terminal amino acids corresponding to mature MGP-A and Gram-negative bacteria, fungi and viruses, specifically Gram-positive and Stam-negative bacteria, fungi and viruses, specifically Staphylococcus arreus, Eschrichia coli, Candida albicans, used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and supplies (claimed). They can a preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 gtgccccgcagtgagtggagggcctgccatccgagtgctctagccgcctggggcaccca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgitgitigocigitgototocottgocotcottgggtotggcaacctcotgcagtttcatc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial (poly)peptide(s) from bowine.and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             supplies (claimed). They can also be applied to crops to reduce post harvest spoilage or expressed in transgenic plants to increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 gigococogoagigagigaggggcocigocalocgagigototaggcgcotiggggcaccca
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α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                They have low immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 677 BP; 146 A; 217 C; 171 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 523.4; DB 18
Pred. No. 4.9e-148;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 5; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95,3%;
98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.4 Matches 540; Conservative
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Murine granulocyte peptide A precursor cDNA.

(first entry)

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AAT78510;

AAT78510 standard; cDNA; 677

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